

#6

Figure 1

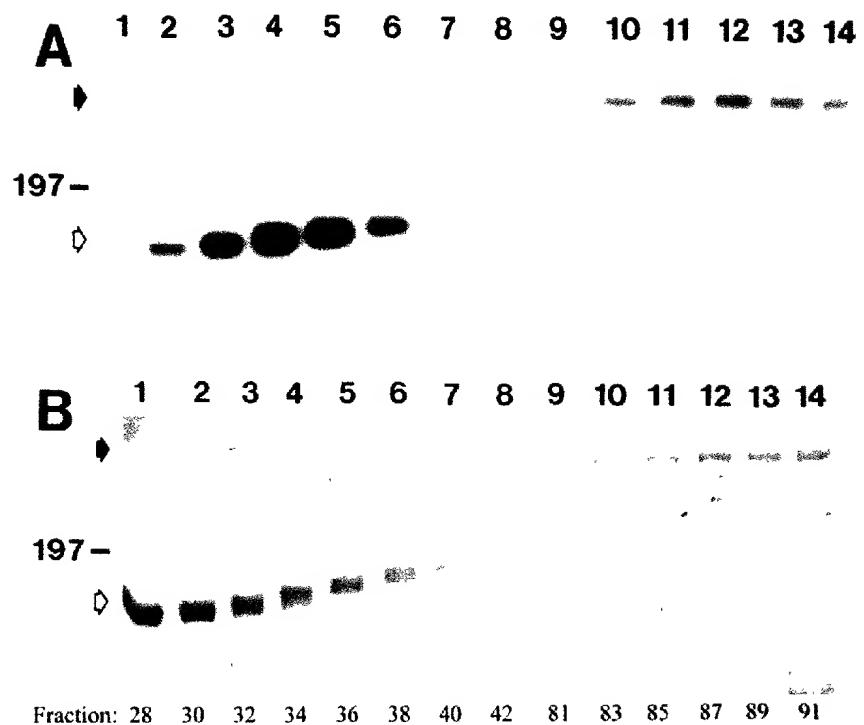


Figure 2

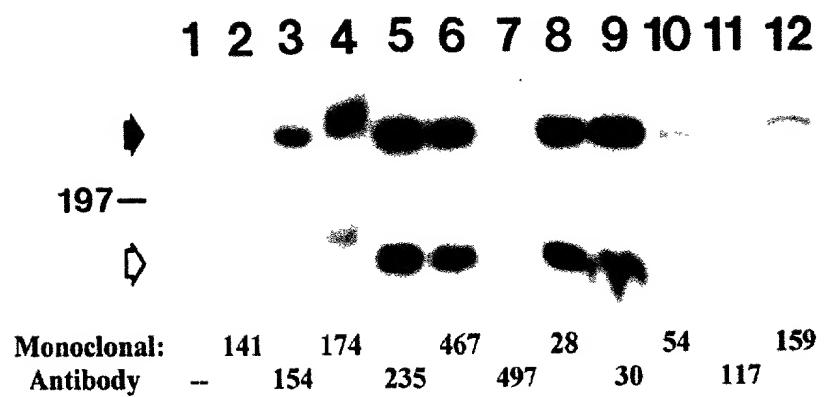


Figure 3

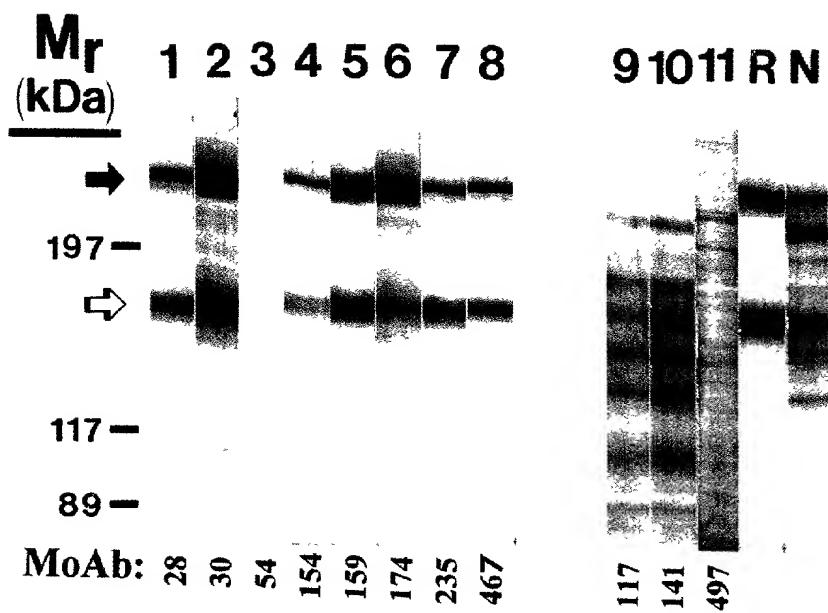


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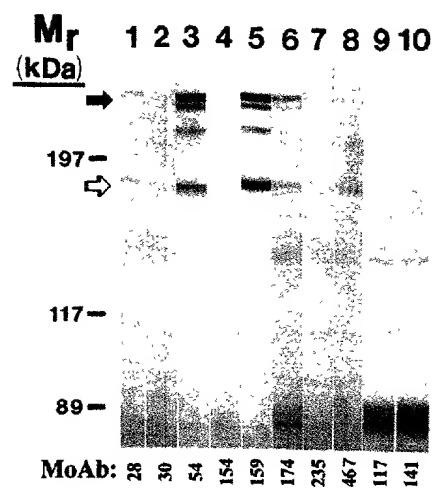


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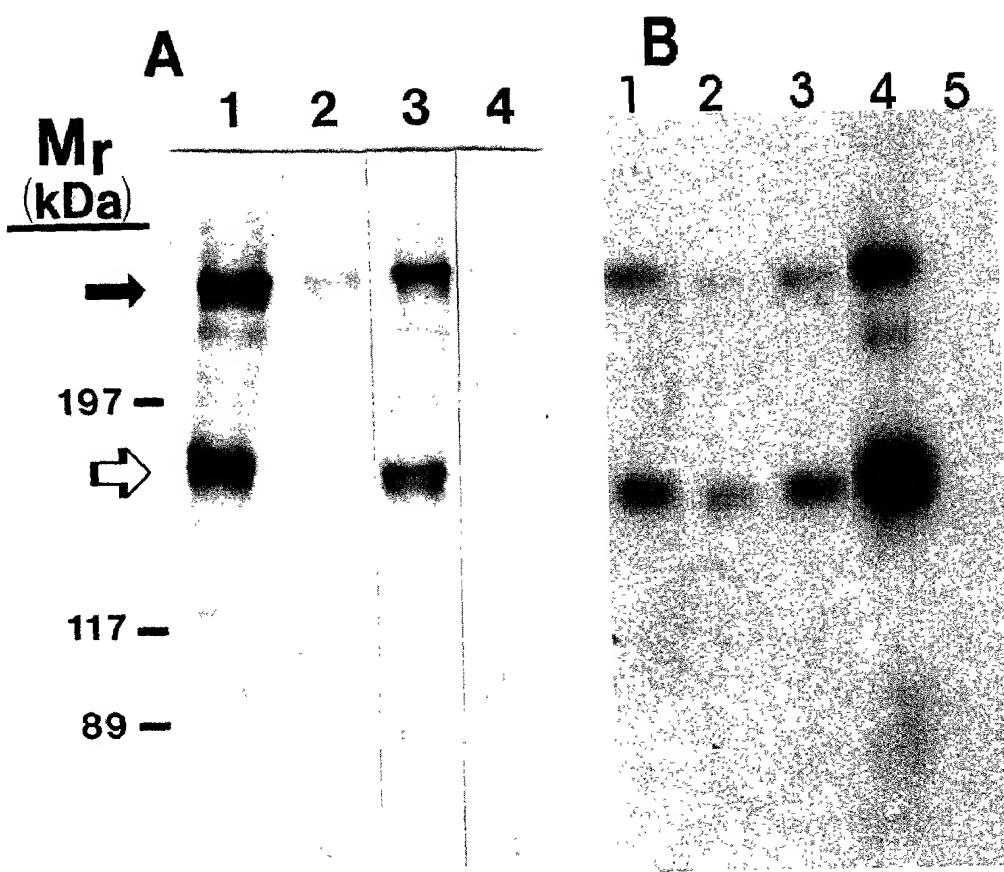


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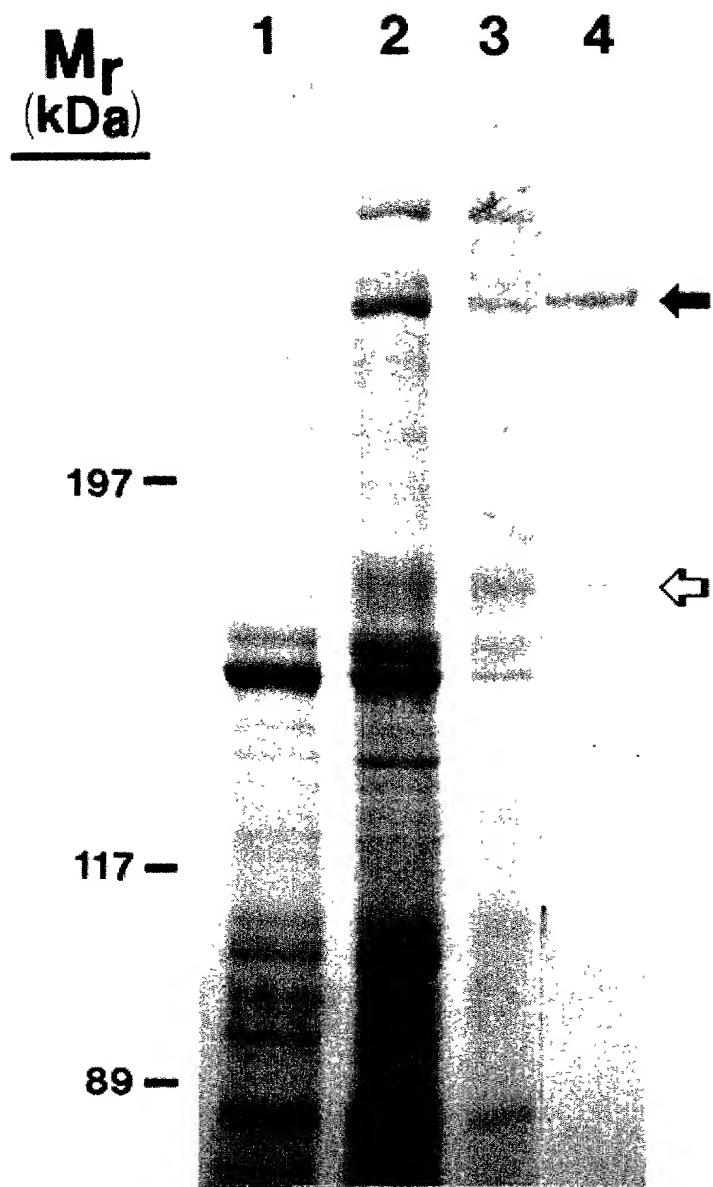


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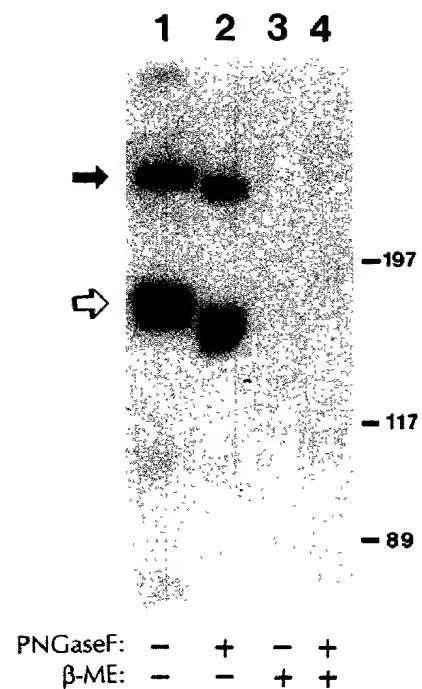
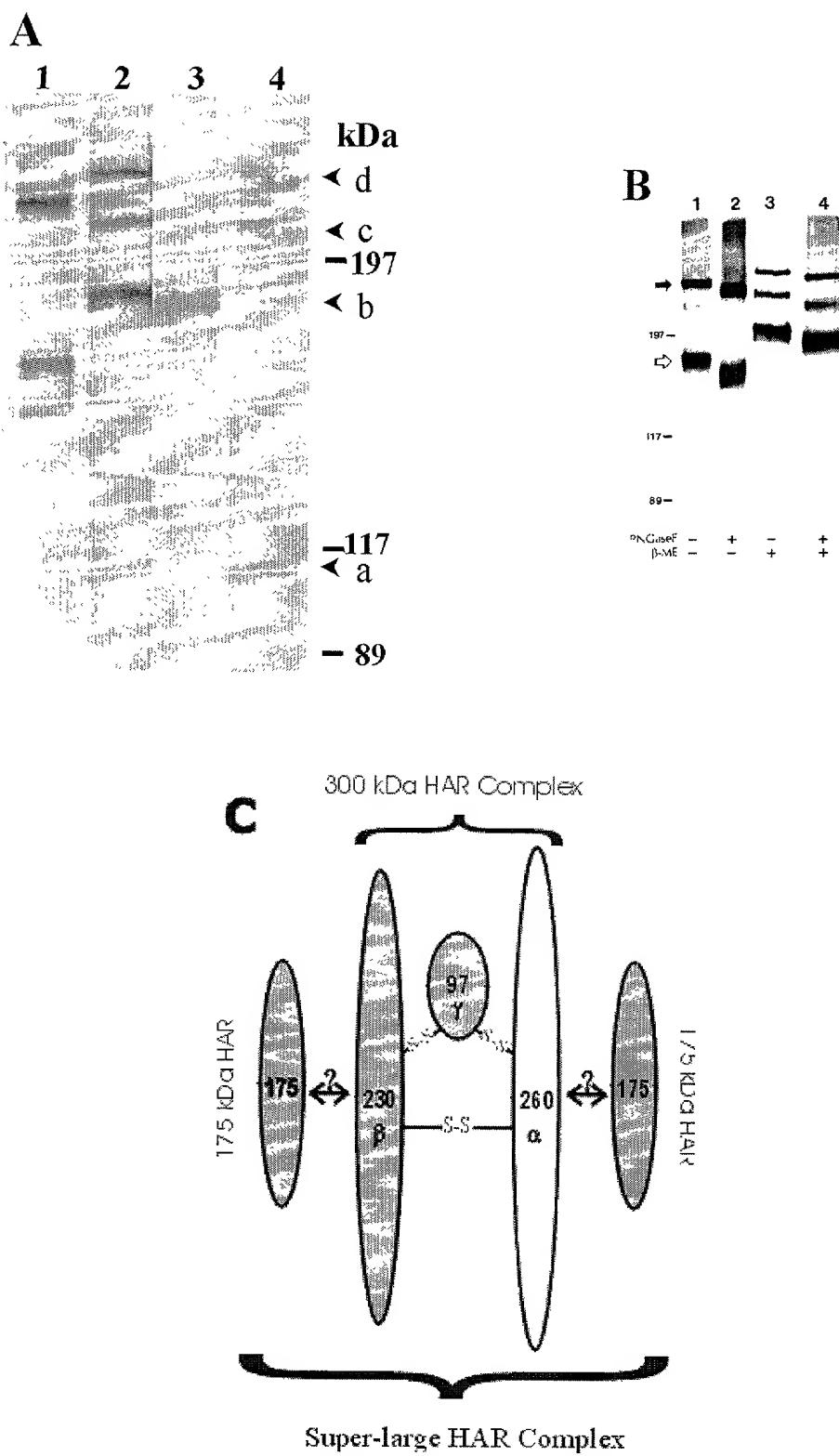


Figure 8



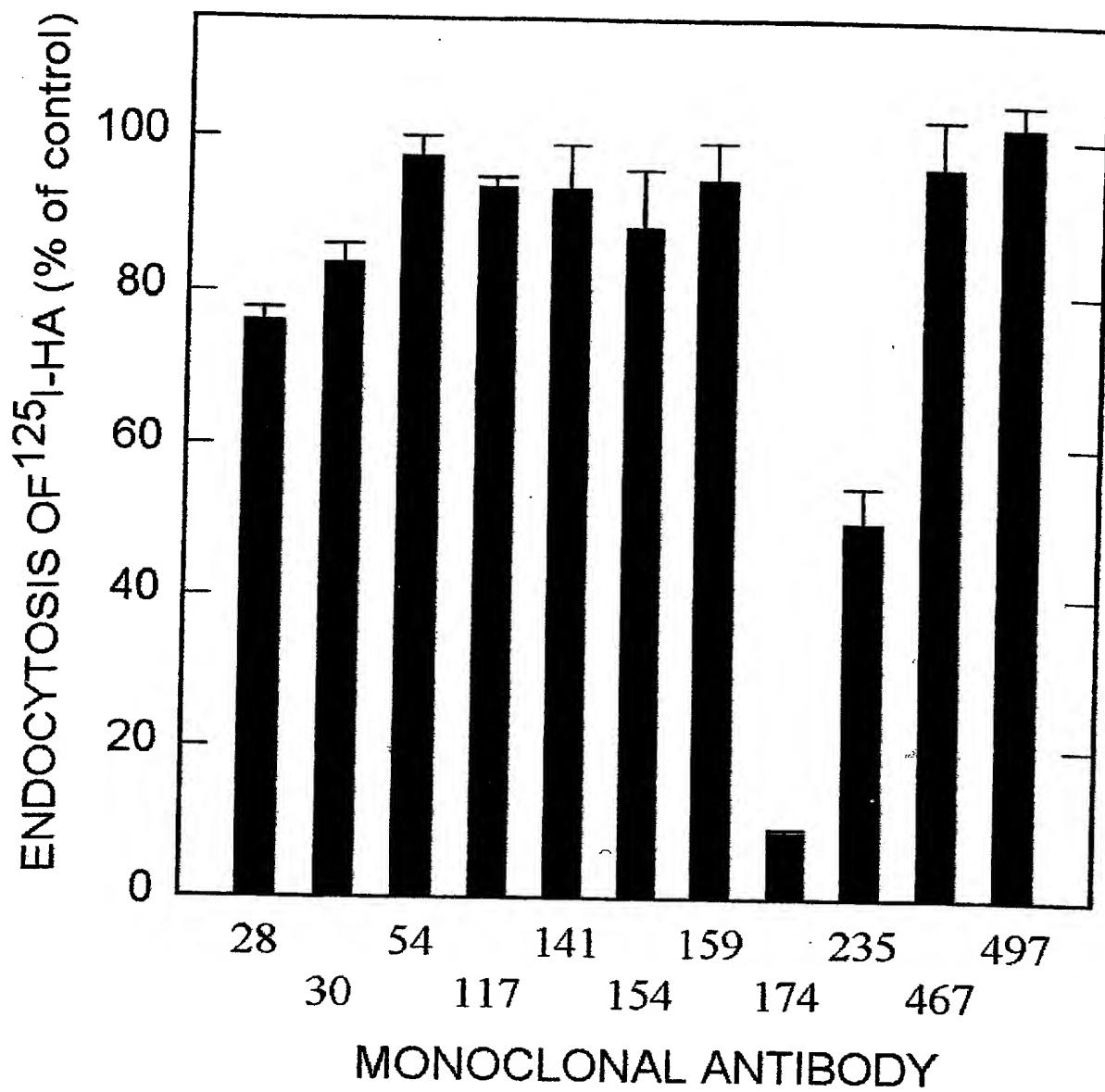


Figure 9

Figure 10

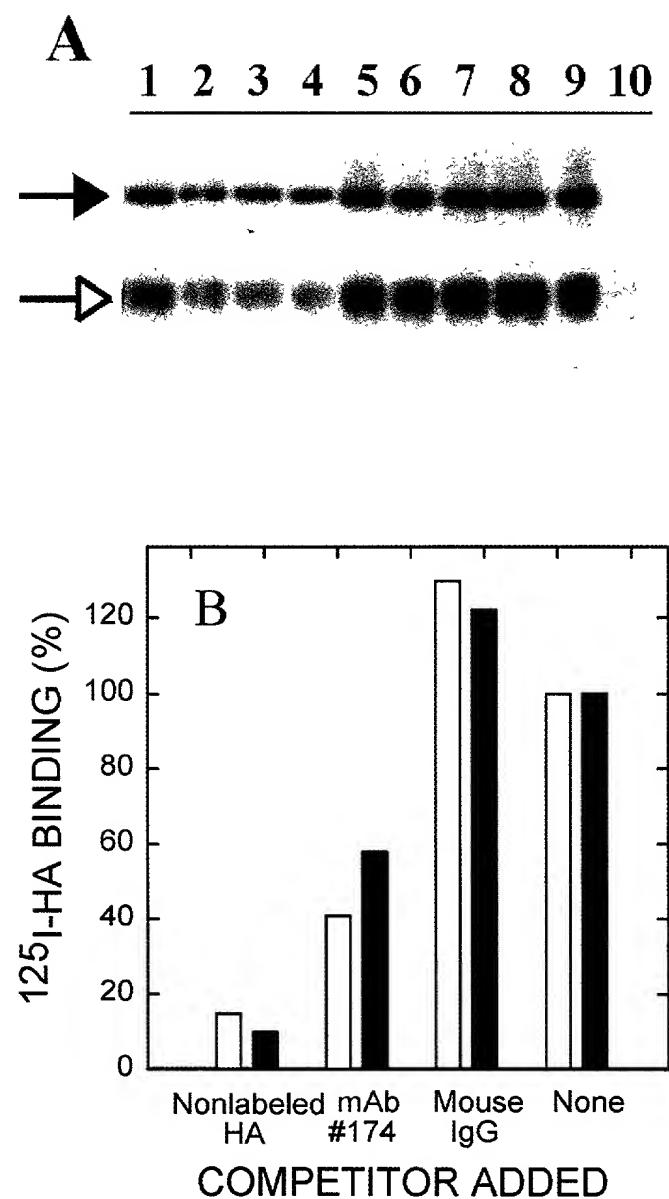


Figure 11

**Antibody Inhibition of HA
Endocytosis by HARE in LECs**

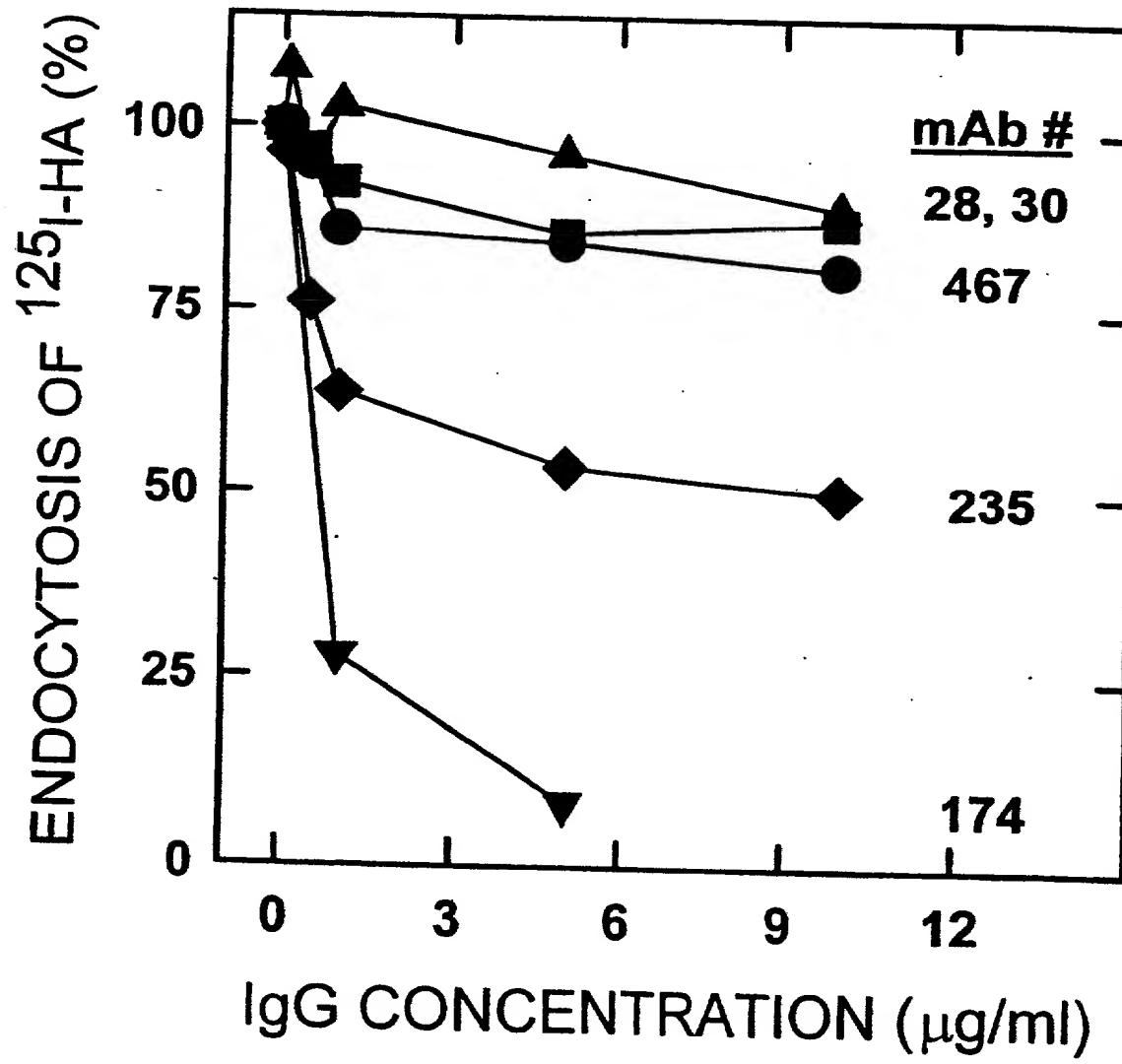


Figure 12

**Antibody Inhibition of HA Binding to HARE
on LECs is Temperature Dependent**

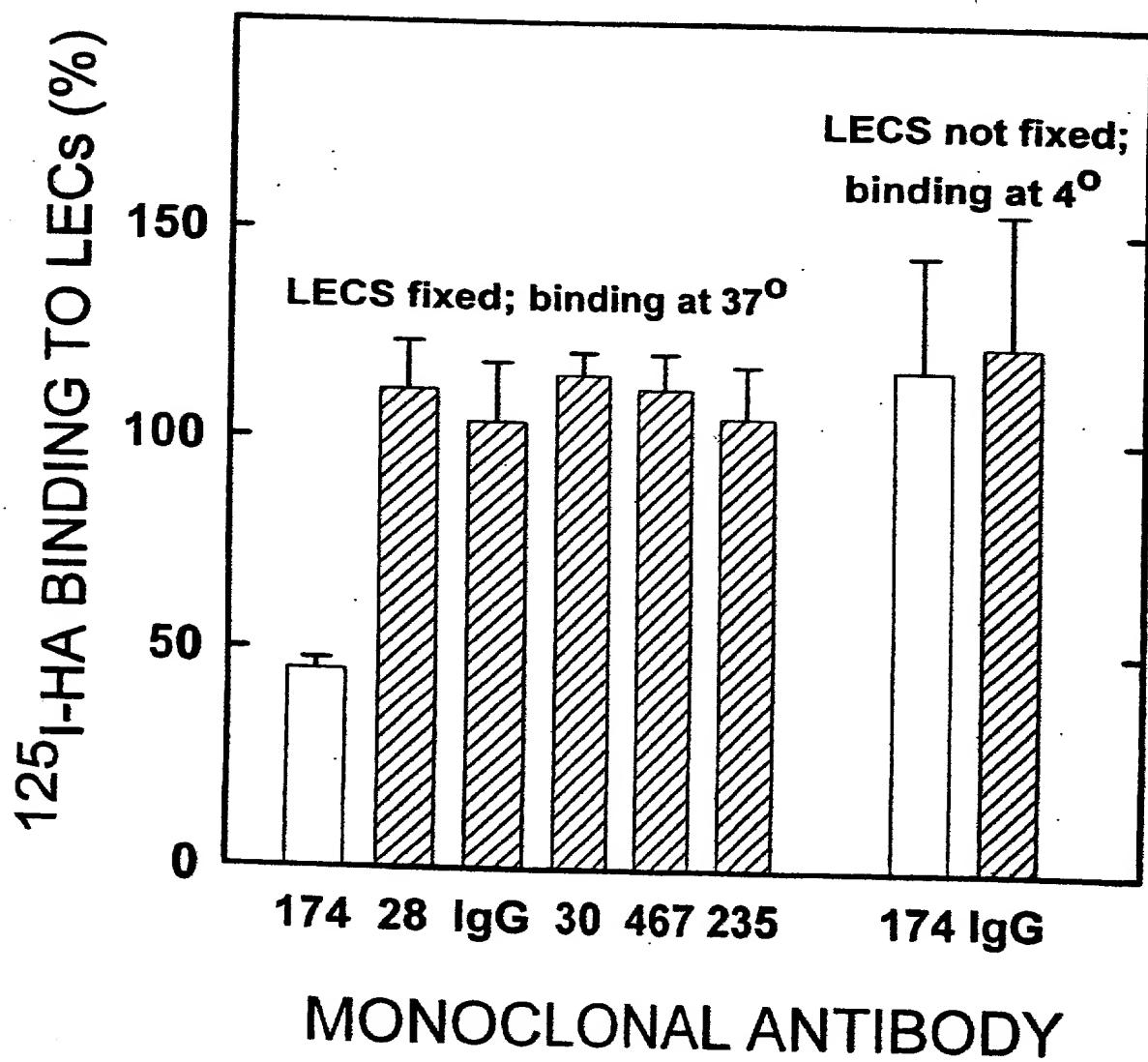


Figure 13

Figure 13

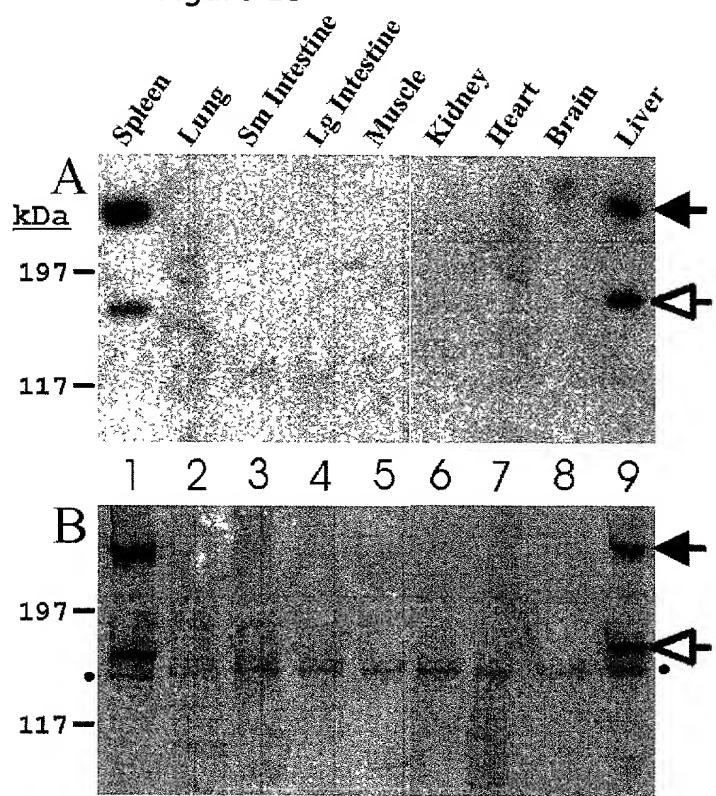
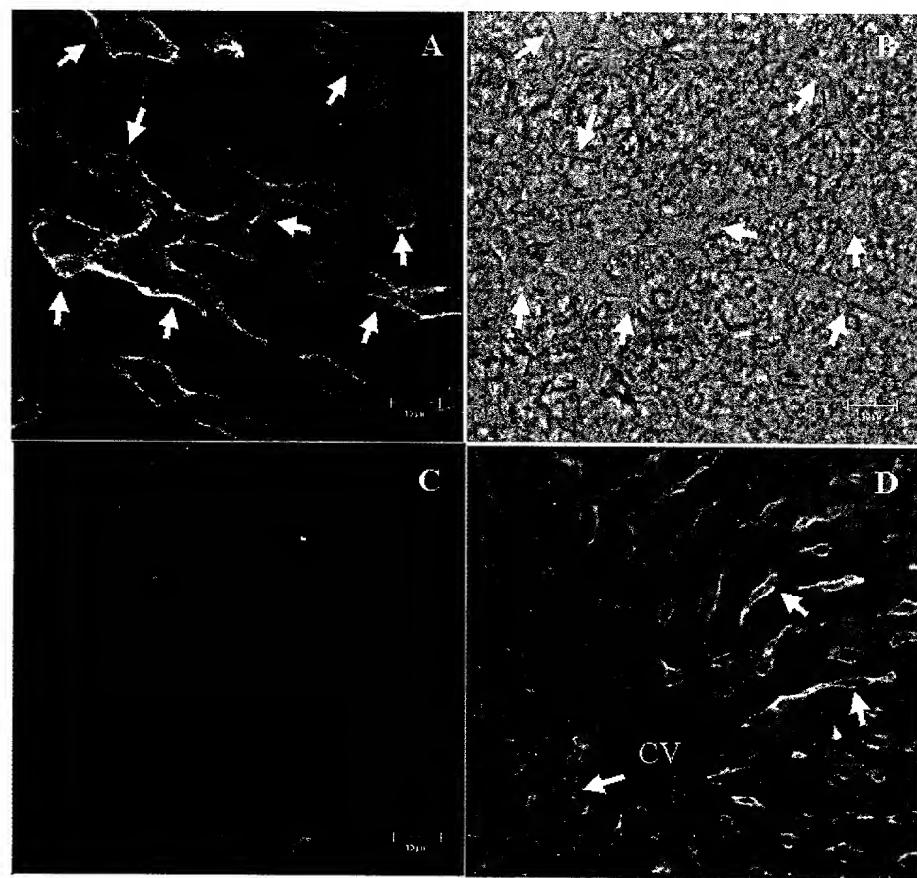


Figure 14



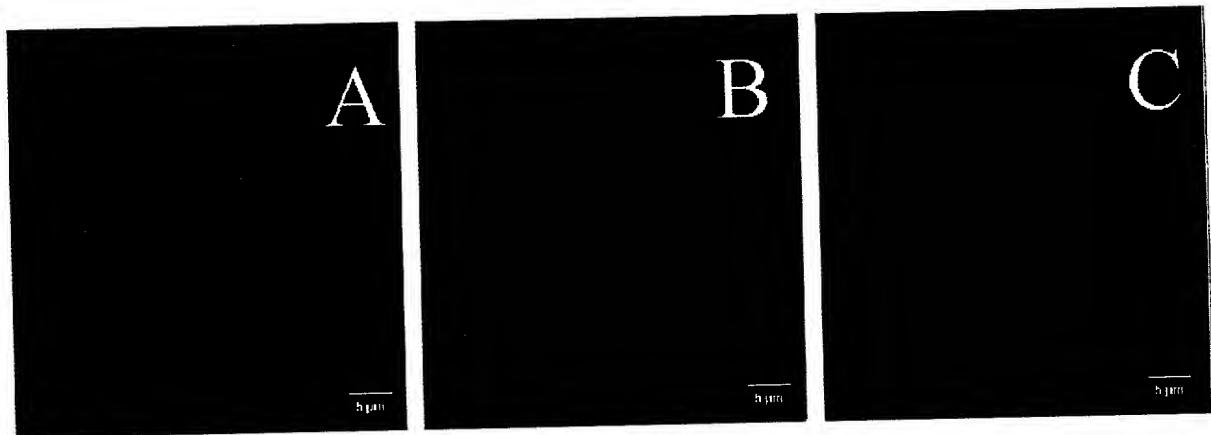
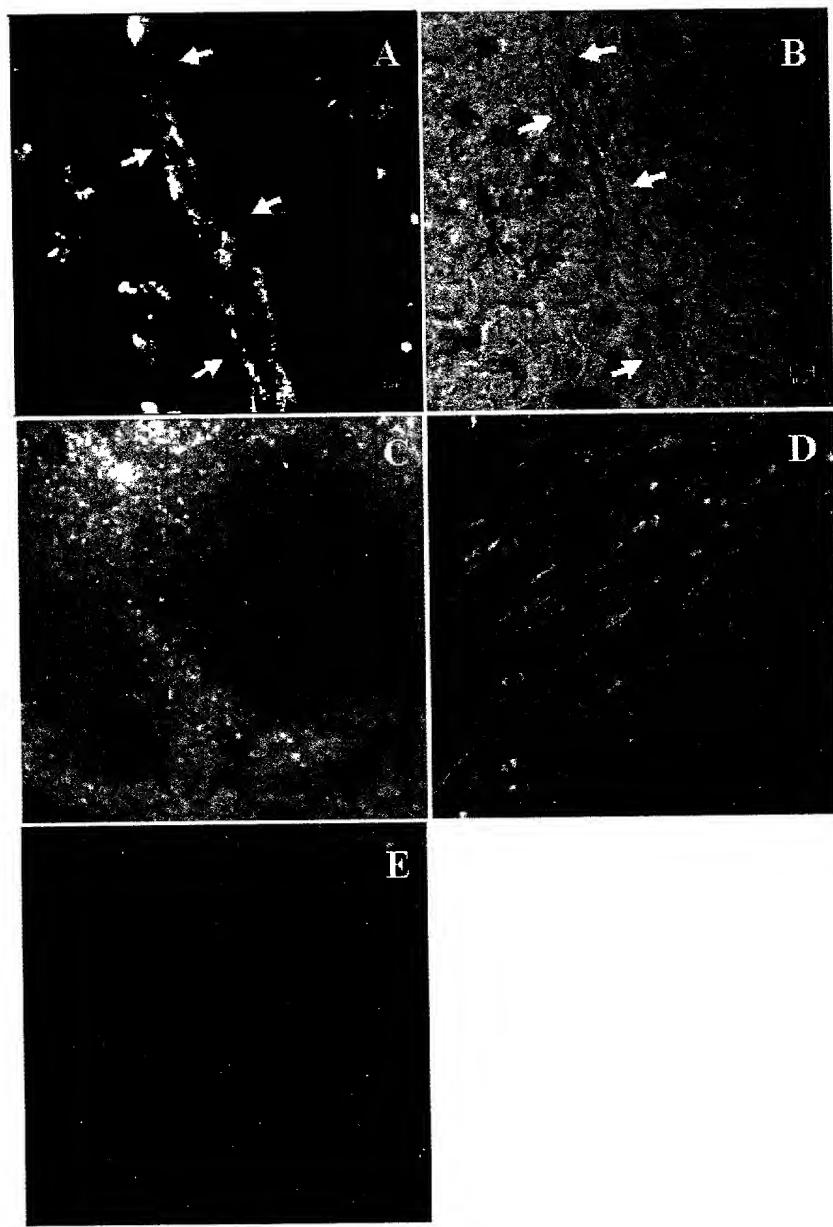


Figure 15

Figure 16



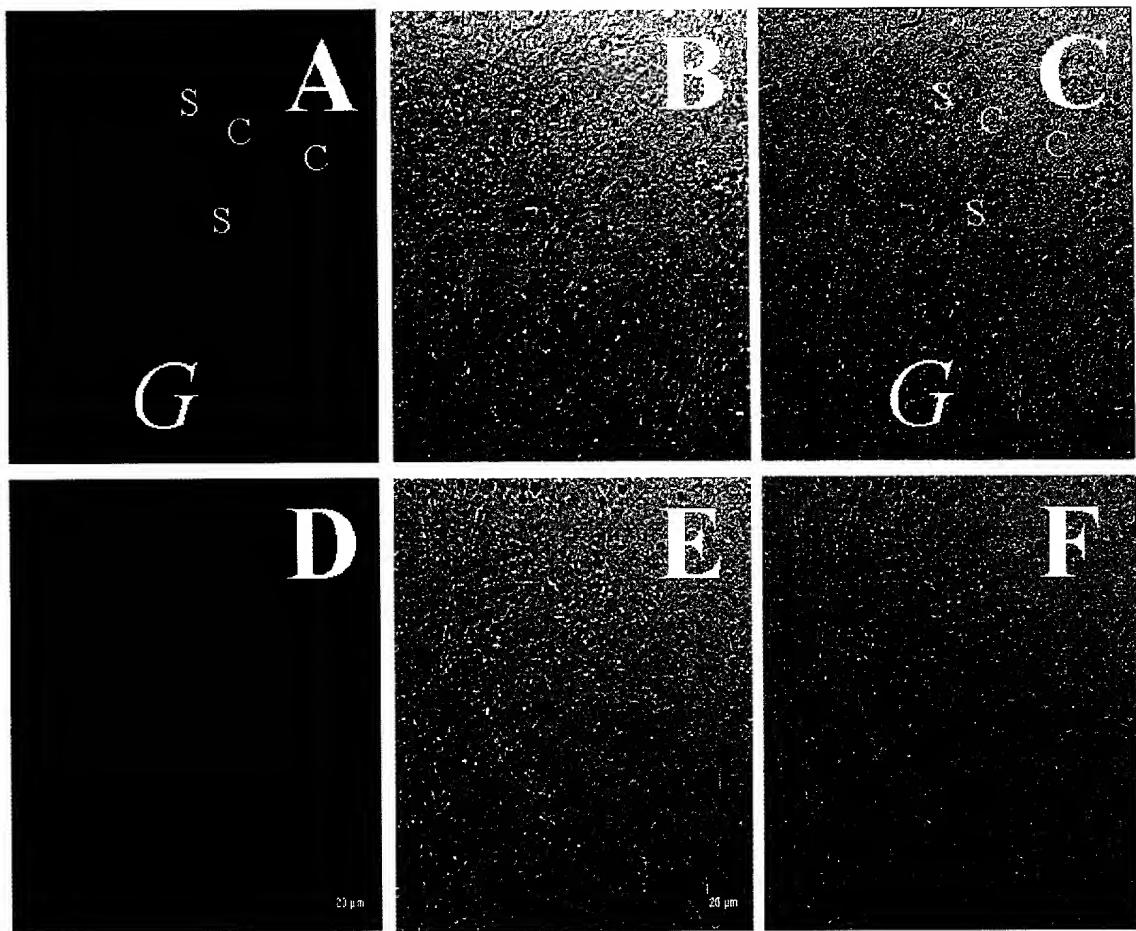
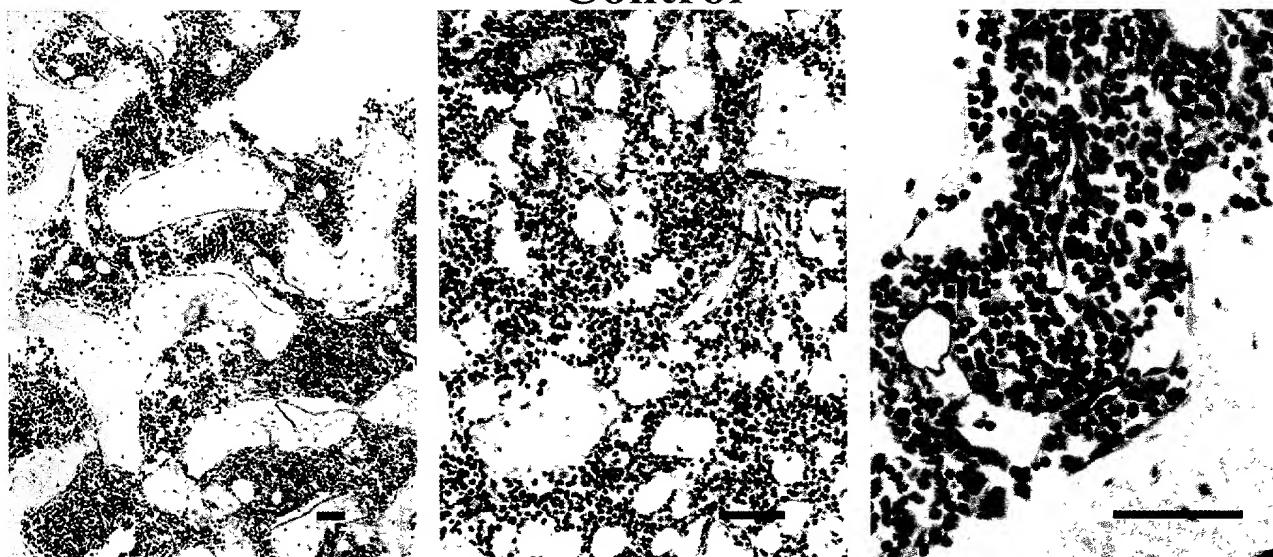


Figure 17

Figure 18

**Immunolocalization of HARE
in Bone Marrow**

Control



Bars = 50 μm

Figure 19

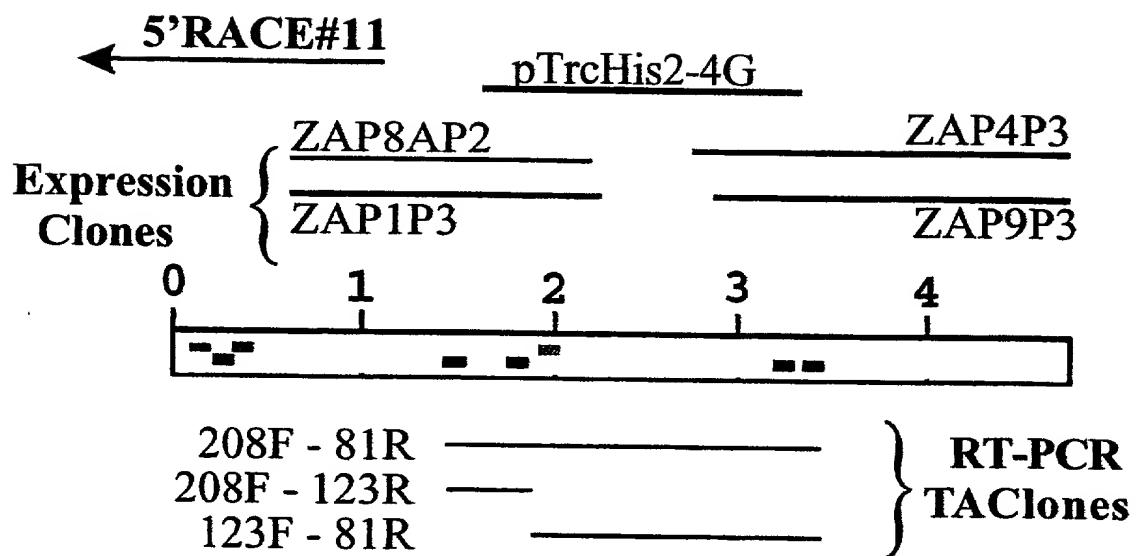


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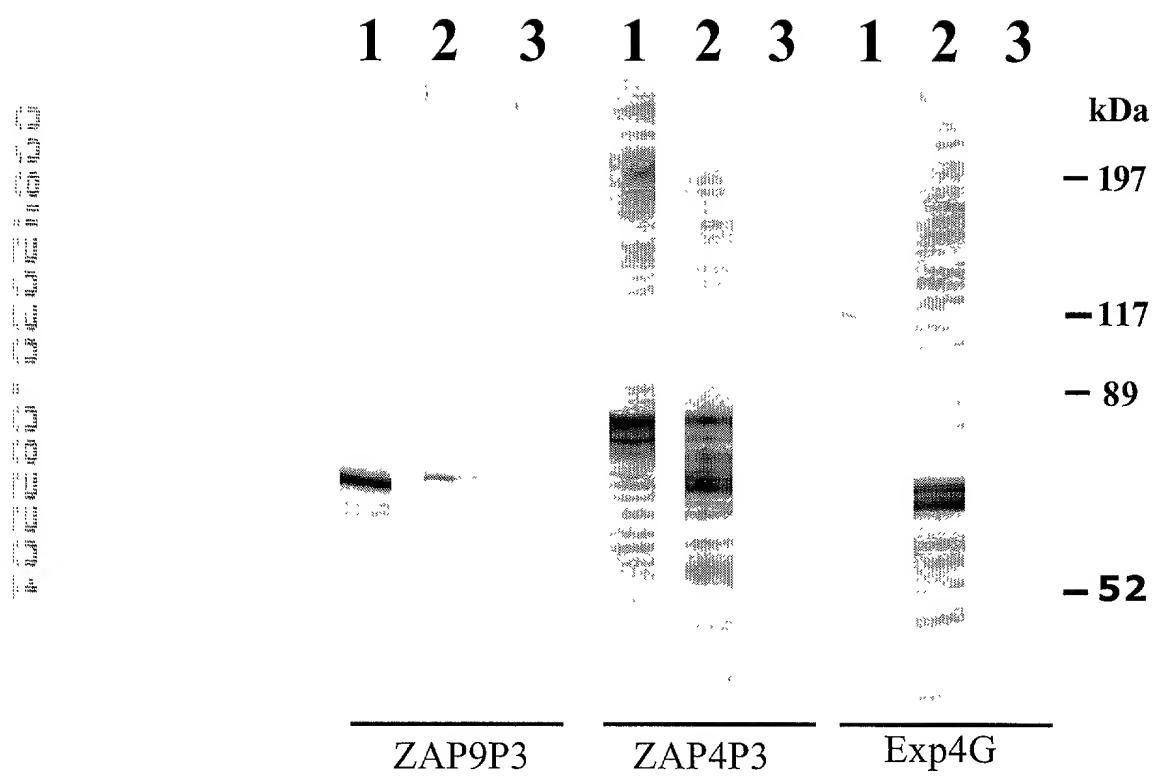


Figure 21

Figure 22

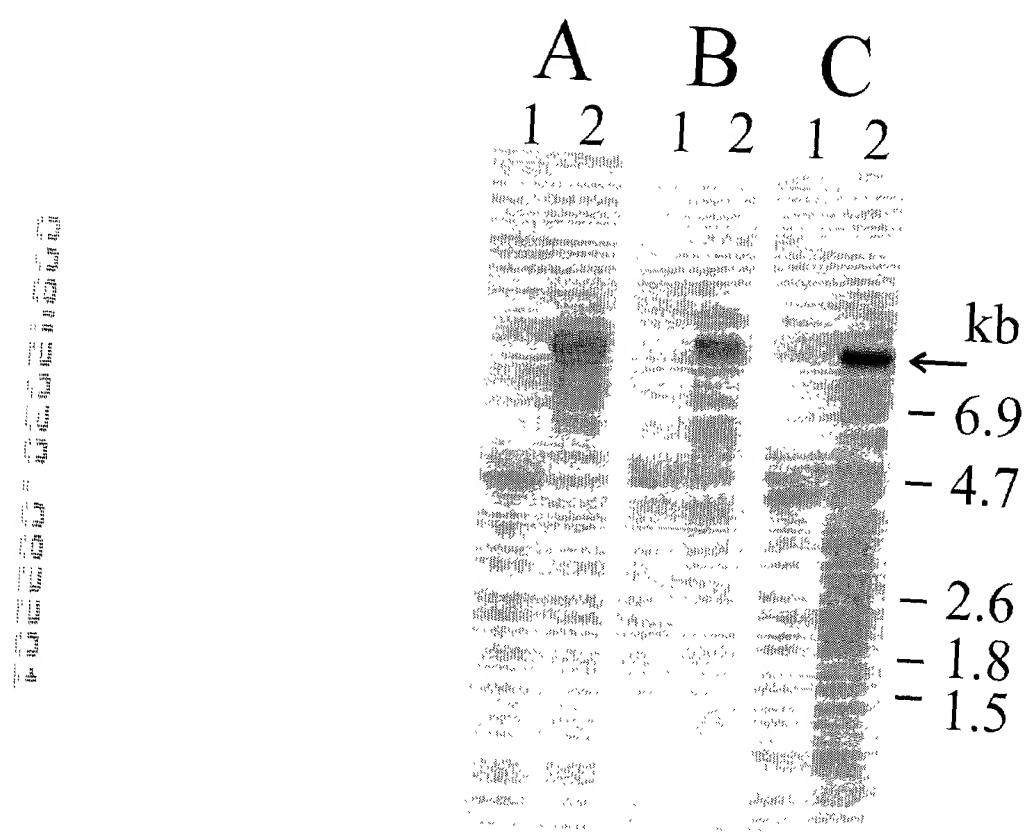


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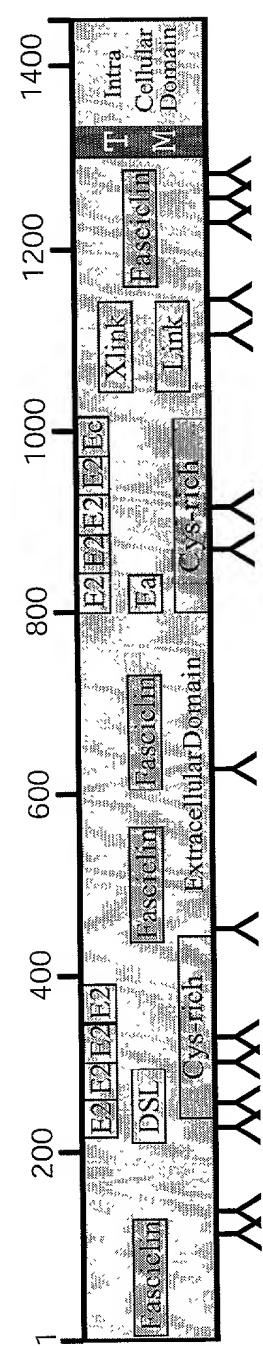


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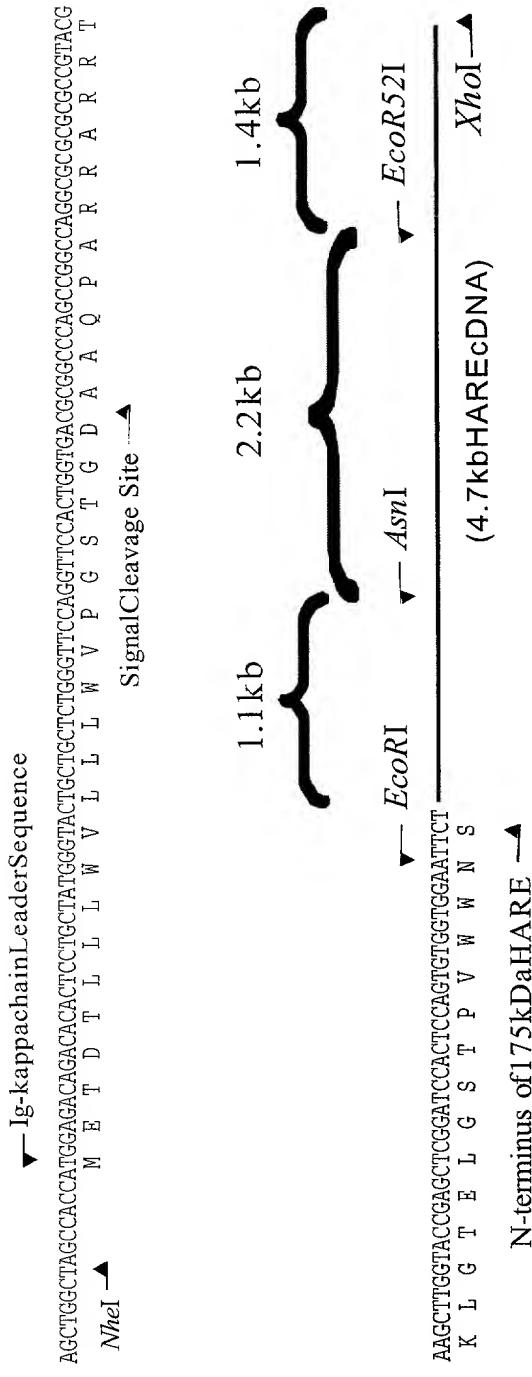
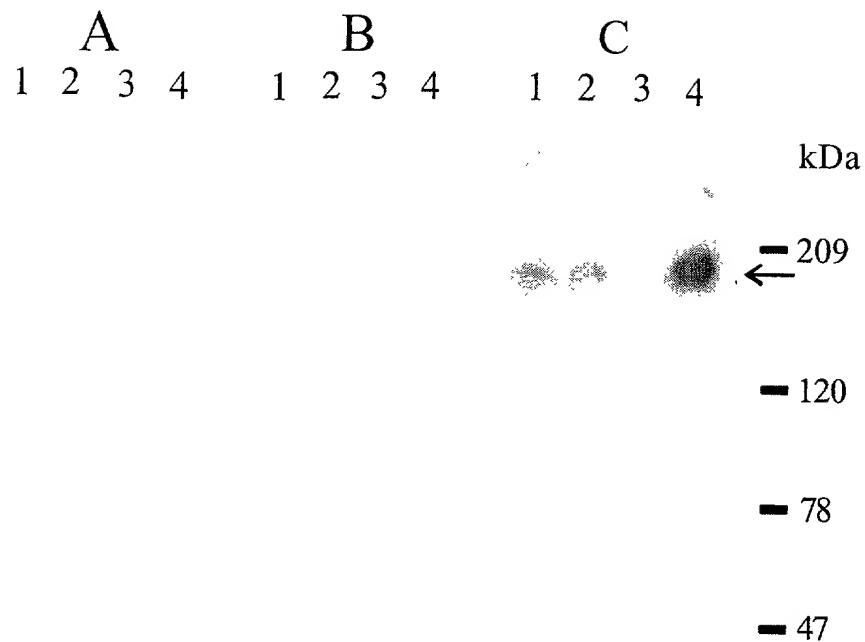


Figure 25

Autoradiography



Western Blot

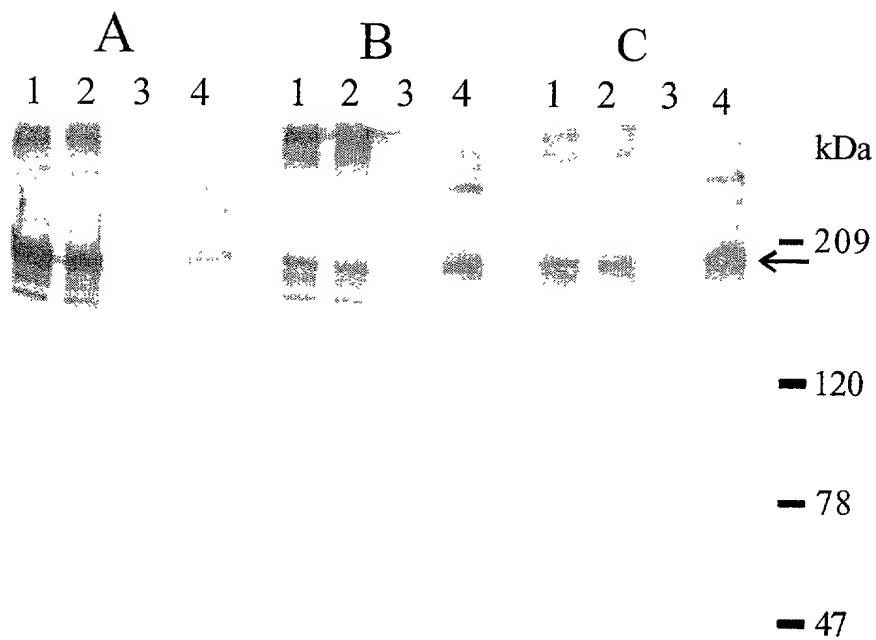


Figure 26

A	B
C	D

Figure 27A

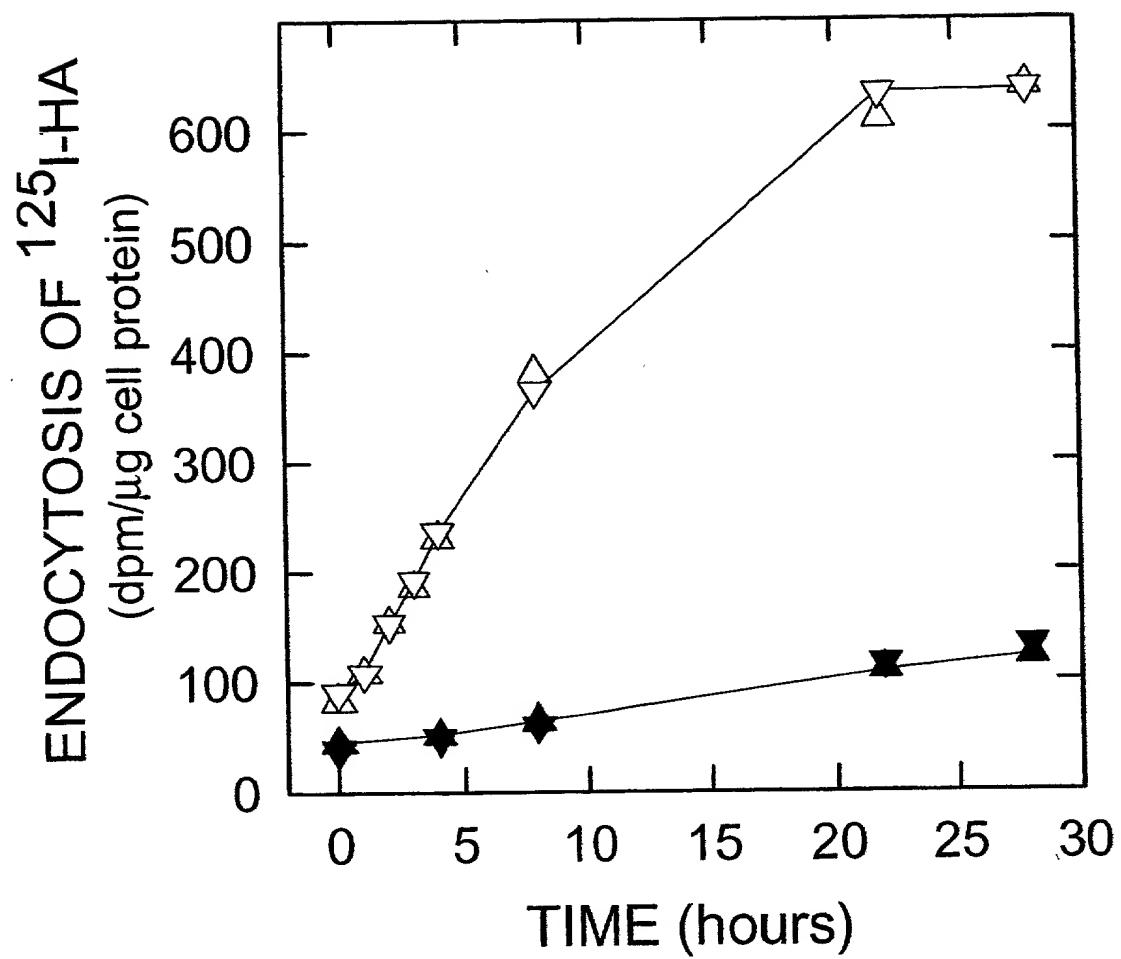


Figure 27B

Degradation of internalized HA by transfected SK-Hep1 cell lines expressing the 175-kDa HARE

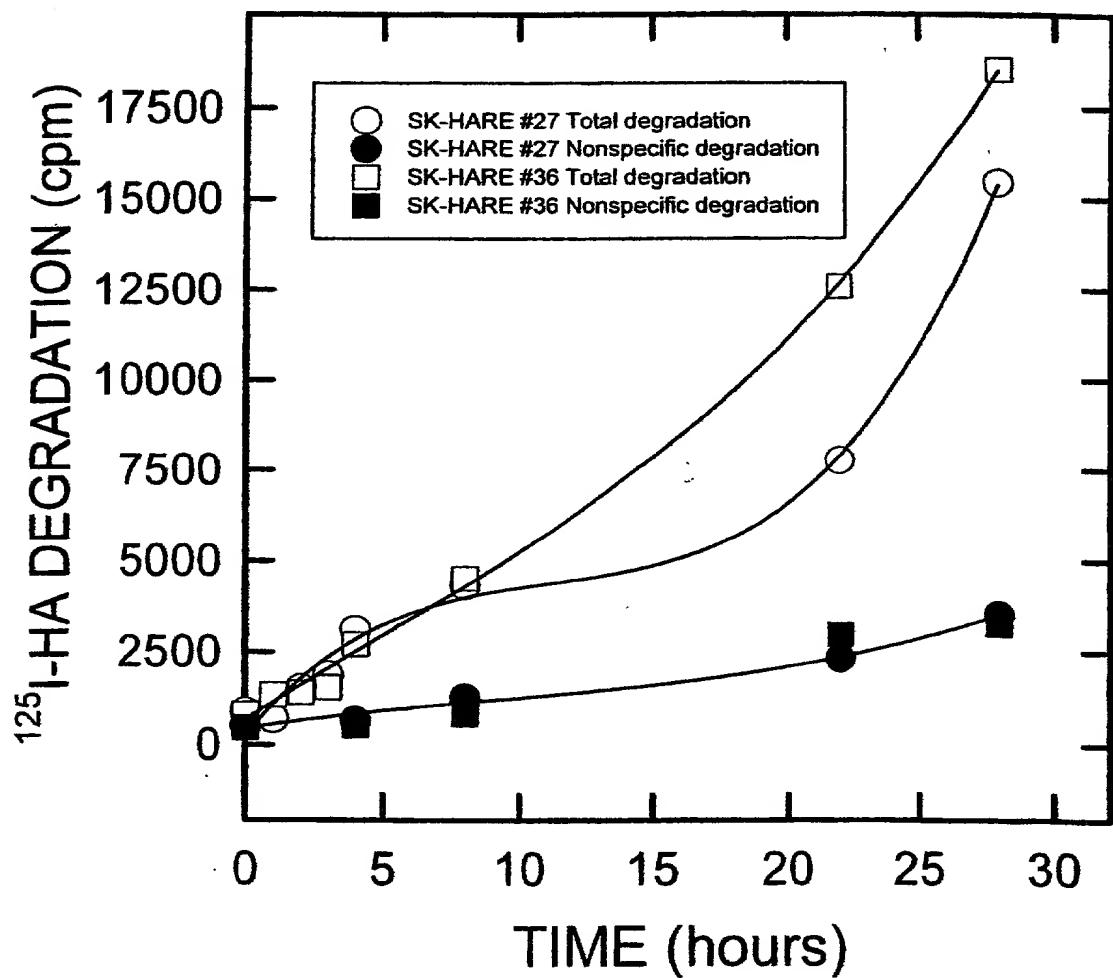


Figure 27C

**Hyperosmolarity inhibits HA endocytosis
mediated by HARE in transfected SK-Hep1 cells**

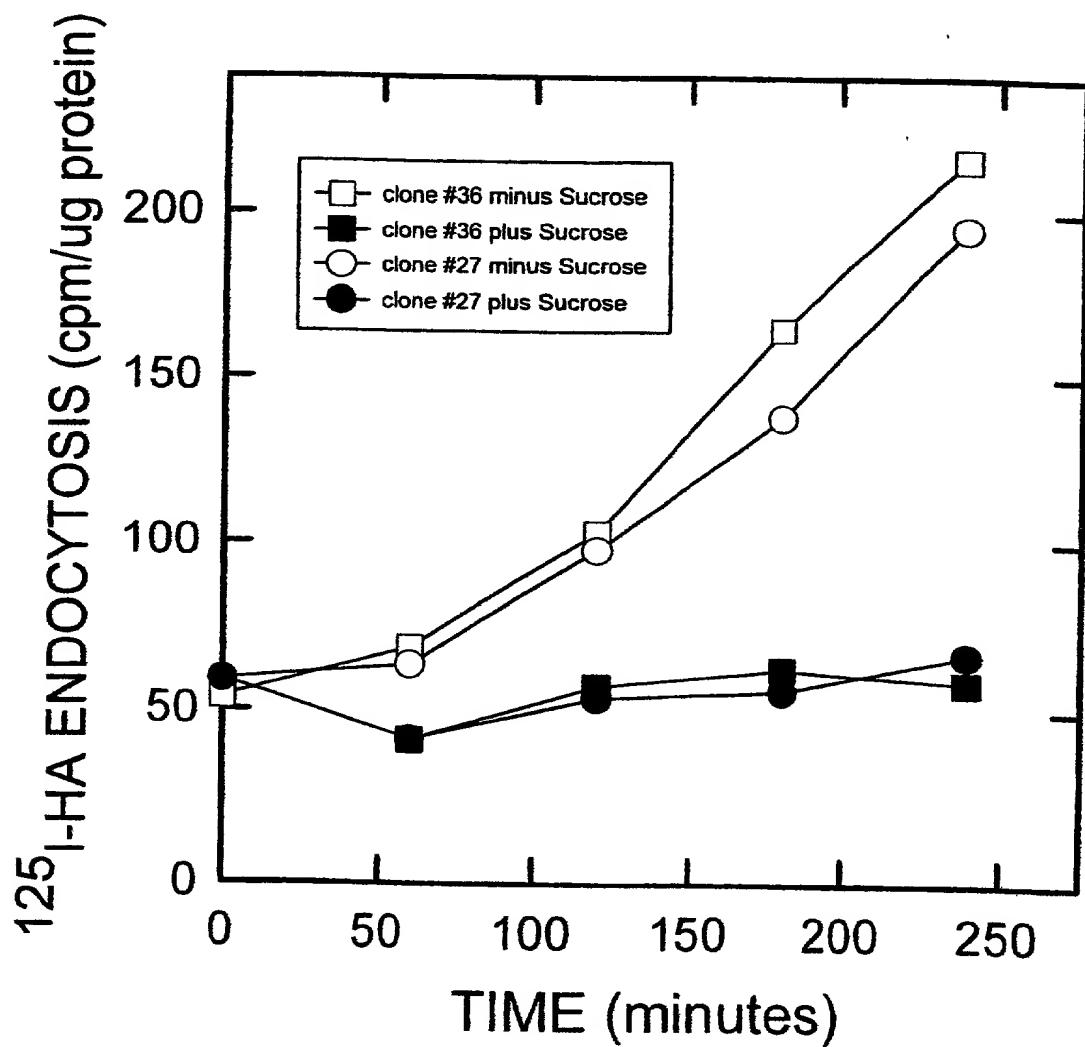


Figure 27D

Specific monoclonal antibodies against HARE inhibit HA endocytosis in SK-Hep1 transfectants expressing the 175-kDa HARE

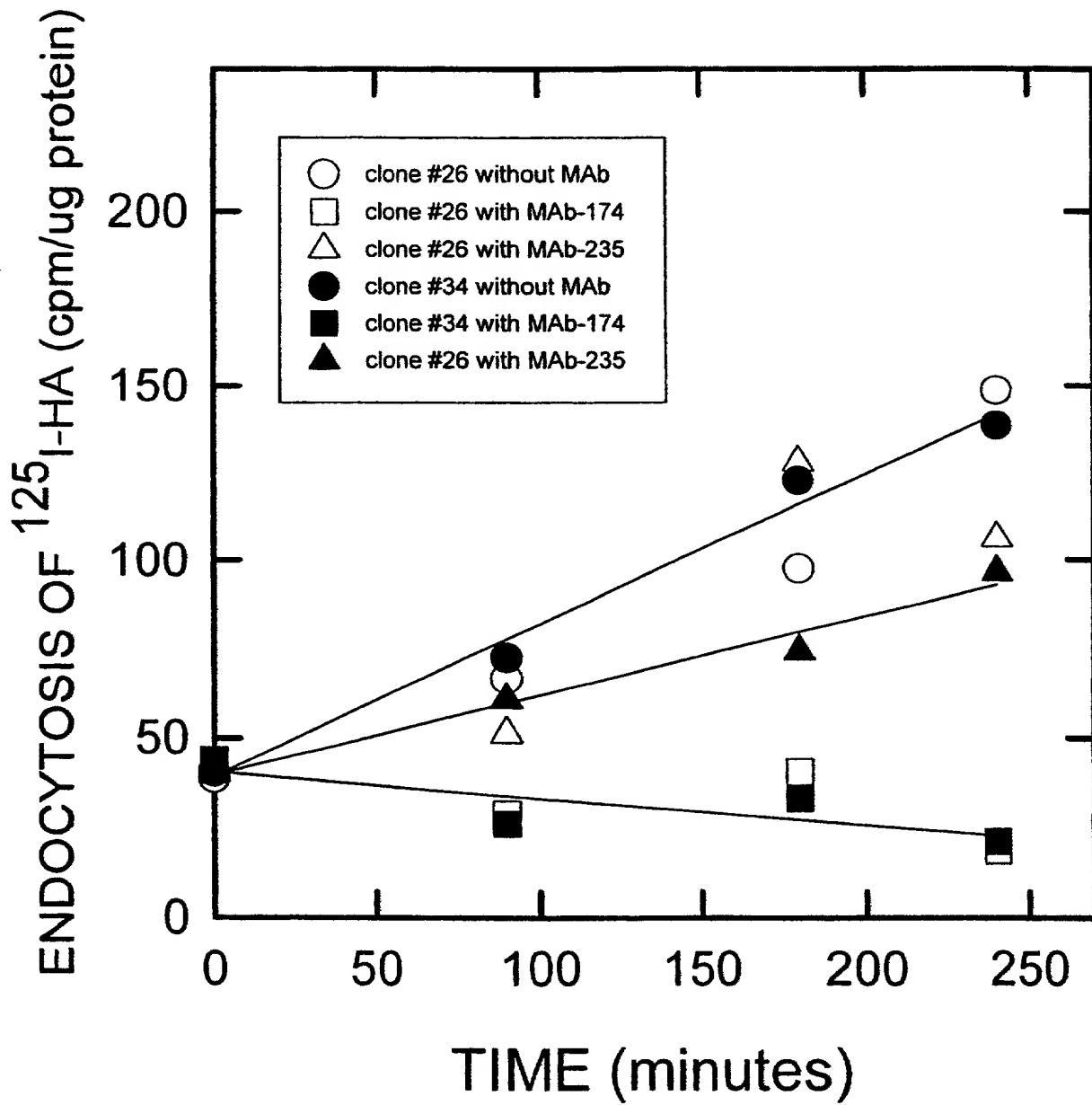


Figure 28

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1111 LHLSQVLLP PRDVPGGCG LLQLDLVPA FSLPRELLOH HGLVQIPEA TAYTIFVPPN RSLEA---QG NSSHLADTV RHHVVLGEAL SMETLRKGH RNSSLGPANH
754 LHLSQVLLP PRGDVPGGCG LLQLDLVPA FSLPRELLOH HGLVQIPEA TAYTIFVPPN RSLEA---QG NSSHLADTV RHHVVLGEAL SMETLRKGH RNSSLGPANH

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1218 IVFVNHSQGP EVNHVPLEGP MLEAPGRSLI GLSGVLTVGS SRSLSHAE LEKGVNTR RFRFTQGQFOL QDTRKSVY RGCFSSR-- --G-SYTRAK KIQVPCDCRG
861 IVFVNHSQGP EVNHVPLEGP MLEAPGRSLI GLSGVLTVGS SRSLSHAE LEKGVNTR RFRFTQGQFOL QDTRKSVY RGCFSSR-- --G-SYTRAK KIQVPCDCRG

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1 ----- W HLRGWS---DG TGVI CGEGF SSTAETTE GKGYIH DDA SIVHGRISQ GPLGDCS D DVGRWRGVHD NATTEDNING THITSANLL
-----VG
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90 NSDGTASAK AAGPFQGNTV STAINAKES NGG-STAKA KRITTEGRNRV TKGAGTYGDD IVLEINPNU ENHGCDRNN BTQZGPNQA ACPVLPATV DG-KVTSLLN
3 EAUTGASKO AAGPFQGNTV STAINAKES NGG-STAKA KRITTEGRNRV TKGAGTYGDD IVLEINPNU ENHGCDRNN BTQZGPNQA ACPVLPATV DG-KVTSLLN
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1076 DSAGASTKA AGYSGNCIF SEVEDPAHG HGGCSPAN TKVAPQRDR TQDGYMGDS DQEINSL IHHCQGHIHA PIPGPOOV SIREGYSQ DGIRTELLD

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112 VLTINNGCS EFAIHTHIG VERIPTKPN Y-IGEGTTR GSIYGEPLKN PTSQYFFQL QEHIVKDLV PGPFITVFAF --LSAAPDEE ARVKDWIYQ IMPQVLRYHV
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1543 PSKNNNGCS PYATKSTGD QORTKDTA HTVGDGLTR ARVGLLELLRD KHAS---FFSL RILLEKEWLKG DPPTFVPH ADLMSNLSDQ ELARIRAHQ L---VFYHV
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1648 VCGRLRSELSE LLEQYATAL SGPHLRSELSE EGSYIINDFA RVVSDSHEAV NGILHFDLVR LLPEALHWE PDPAPIPRRN VTAACQGPGY KIFSGLLKVA GLLPFLREAS
1291 VCGRLRSELSE LLEQYATAL SGPHLRSELSE EGSYIINDFA RVVSDSHEAV NGILHFDLVR LLPEALHWE PDPAPIPRRN VTAACQGPGY KIFSGLLKVA GLLPFLREAS

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348 PTLGGRDFN TTFDAS-GEI GS11VNTPS P RSKPKGVK K---IY ---N-LPF K-----RERSLVIOI PRFHGYPGR DQGQFEGGD
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924 LITFS---QD PLQPTETRFV DGRSILQWDI FASNGILHII SRPKAPAP VIL---THIG LGAGIFFIAI LVTVATA-L AAYSYFRINR RTIG-FOHF ESEEDINVA
752 LITFS---QD PLQPTETRFV DGRSILQWDI FASNGILHII SRPKAPAP VIL---THIG LGAGIFFIAI LVTVATA-L AAYSYFRINR RTIG-FOHF ESEEDINVA
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1024 LGKQOPENIS NPLY-ESTTS APPERSYDPP TDSER-----QLEGNDP LRTL
552 LGKQOPENIS NPLY-ESTTS APPERSYDPP TDSER-----QLEGNDP LRTL
CAB61827
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Figure 29

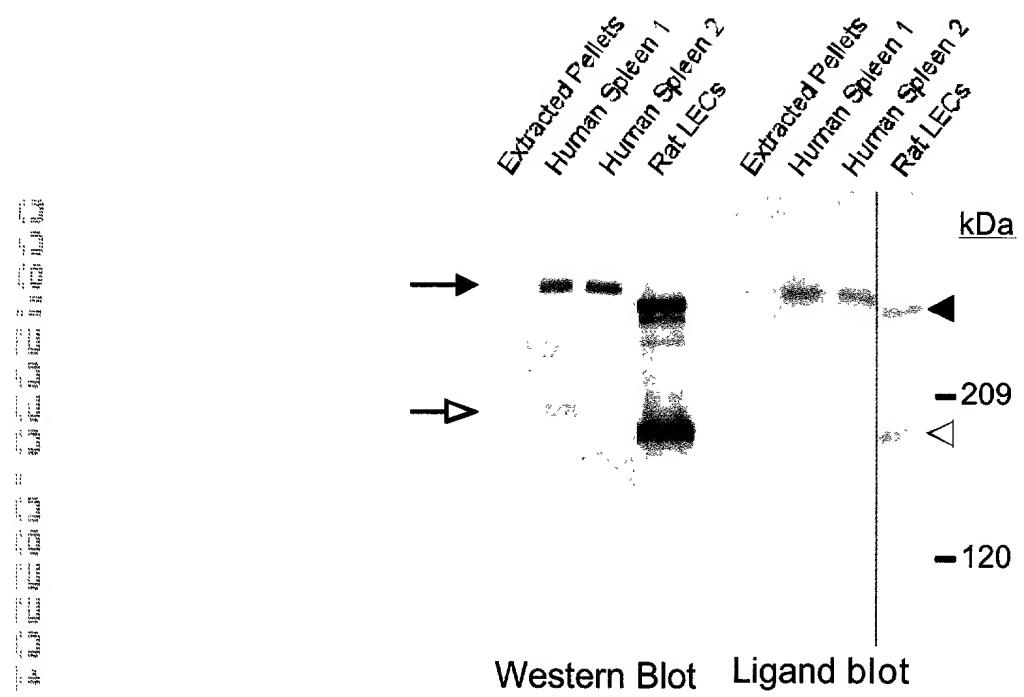


Figure 3 0

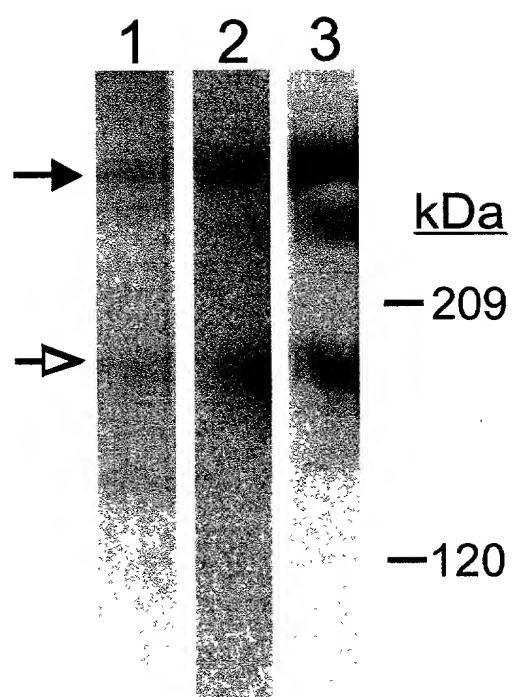


Figure 31

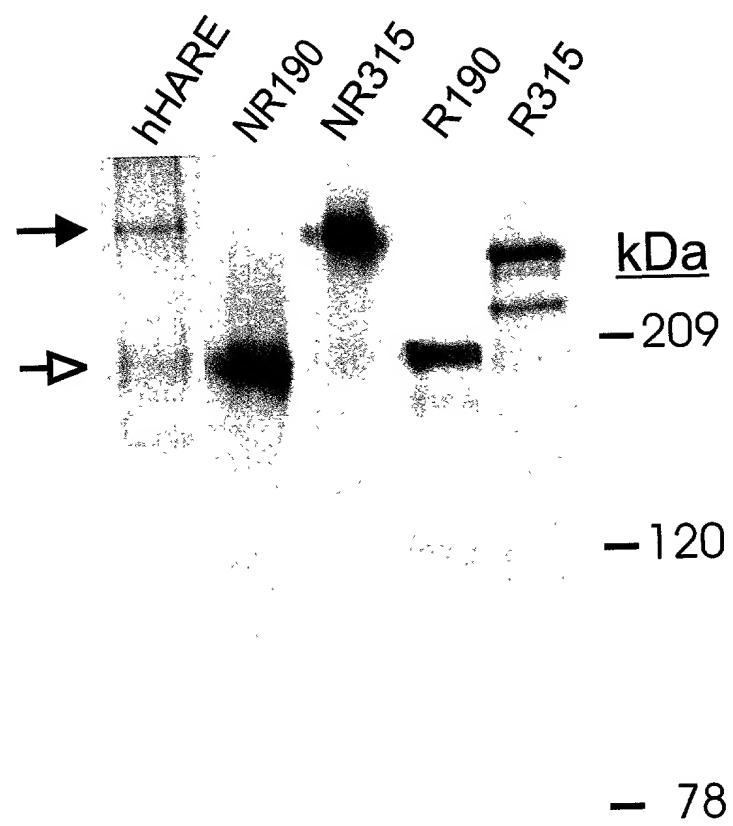


Figure 3 2

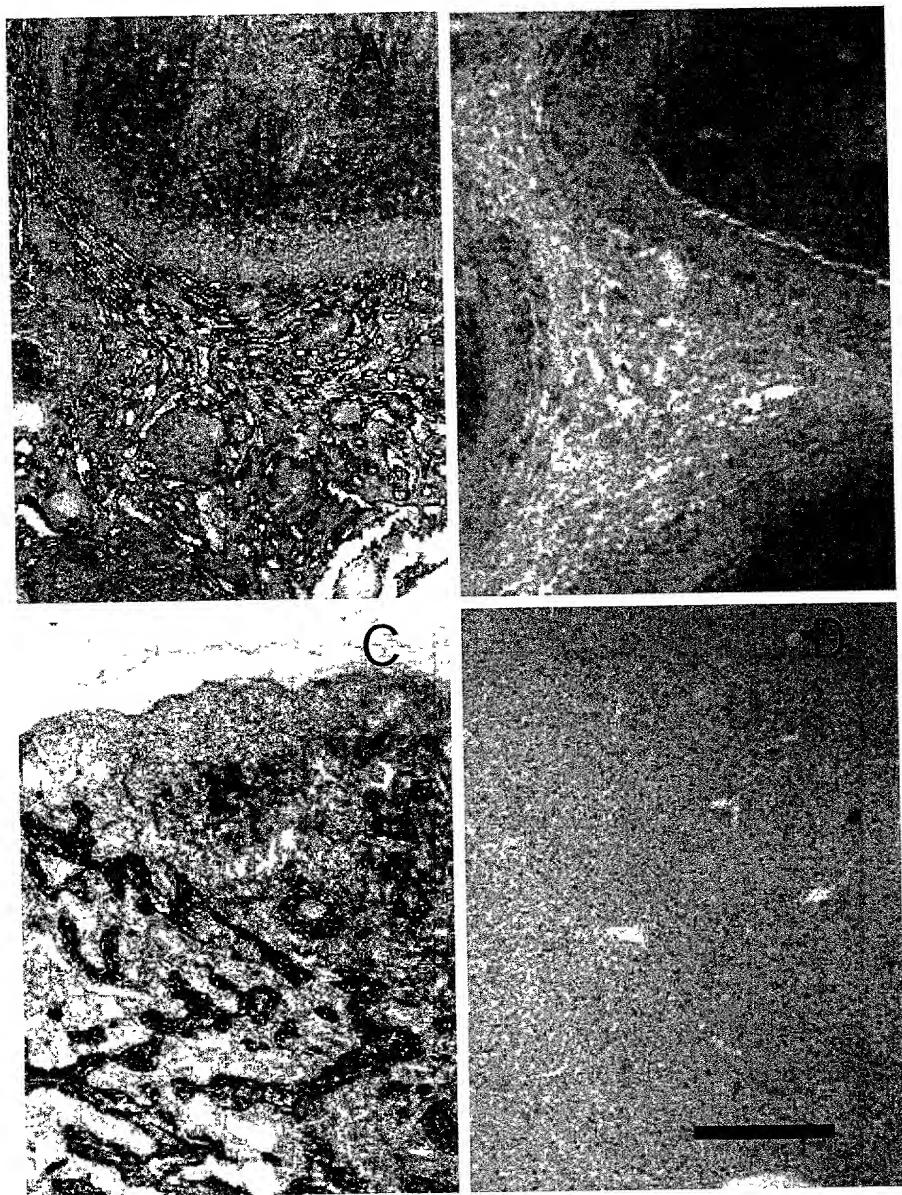


Figure 33

1 ATTCAATATAATCTGGCGAATGCAATTGAGGTGCGCATGCCATCACAGTGTGTCACAAACATGCCATCGAGAATTACATCAGGGAGAAGAAAGTCTGTCAGGGAGGAC
 1 N L A N A I E A A D A Y T V F A P N N N A E N Y I R E K V K V L S L E E D
 121 GTCTCCGGTATCATGGTCTGGAGGAGAACCTCTGAGAATGAGCTGCACATGGCATCGAGGACCATGCTGGGTTCTCCATTTCCCTAGCTTCATGAC
 41 V L R Y H V V L E E K L L K N D L H N G M H R E T M L G F S Y F L S F F C H N D
 241 CAGCTCTATGTAATGAGGCTCCAATAAACATACACCAATGAGCCACTGATAAGGGAGTCTGAGGAAATTCTGAGAATTCAGAACACAGATGATAATAGAC
 81 Q L Y V N E A F I N Y T N V A T D K G V I H G L G K V L E I Q R N R C D N N D
 361 ACTATTAACAGGGAGATGAGGACATGCTCTGAGGACCTTGCCATTGGAAACTAATCTCTAGGTAATGAGAGAGGAGATGATCTACCCCTATTCATGGGAAGGAG
 121 T I I R G R C R T C S S E L T C P F G T A S K N E R R C I T T S Y F M G R
 481 ACCCGTTTATGGTGCAGGCCAAATCTGAGAAGCCGCTTACAGAGAAGATGCTGTGGGCTTCTGGCCCCATGCCAGGCCGTGCAAGGGAAATGCCAGAATGCTGCTT
 161 T L F I G Q P C V C R T V I T R E C C A G F G P Q C P G N A Q N V C F
 601 CGTATGGCATCTGTTGGATGGACTGATGGCAAGCTGTTGACTGGGGAGGGCTTCAGGCCACAGGCTGGAGACCTGCACCGGGCAAGTGGCAGCCACTGTGACCA
 201 G N G I C L D G V N G T I G V C E C G C E G F P S G T A C E T C T B G K Y G I H
 721 GCATGGTCTGGTCCATGGGAGATGCAACCAAGGACCCCTGGAGATGGCTCTGTGACTGTGATGTTGGCTGGAGAGTGCATTGTGACATGCAACACAGAAGACAATGCAAT
 241 A C S C V H G R N Q G P L G D G S C D C D V G W R G V H C D N A T T E D N C N
 841 GGACATGCCATACAGCGCCAATGCTCACCACCTAGTGGTACAGCTCATGAGTGTGAGCAGGATTCAAGGAAACGGGACCATGCAACGACATCAATGCTGAGATC
 281 G T C H T S A N C L T N S D G T A S C K C A A G F Q G N G T I C T C A I N A C E
 961 AGCAATGGAGGTGCTGCCAAGGCTGACTGTAAGAGAACACCCAGGAAGGCGAGTGTGACCTGCAAGCAGGCTACACGGGTGATGGCATTGTGCTGGAAATCAACCGGTT
 321 S N G G C S A K A D C K R T T P G R R V T C T C K A G Y T G D G I V C L E I N P C
 1081 TTGGAGAACATTGGTGGCTGTGCAAGAATGCGGGTGCACAGGACAGGACCAACAGGGCTGCTTAAGTGTGGCAGGATACACTGGAGATGGAATTACCTGCGG
 361 L E N N H G G C D K N A E C T Q T G F N Q A A C N C L P A Y T G D G K V C T L
 1201 GTCTGGTCTTAACTAAAATGGCGCTGTGACTGATTTGCCATCTGCAACCAACTGGGCAAGTAGAACGGACTTGTACTTGCACGGAAACTACATGGAGATGGATTACCTGCGG
 401 V C L T K N G P K N H C A P I N H T Q V O R E T C T C K P N Y I G D G F I C R G
 1321 AGCATTTATCAGGAGCTTCCCAGAACCCGAAAATCTCCAGTATTCTCCAGTGTGAGGAGCTTCCTGAGATCTGGTCTGGCCACGGCCCTTACTGACCTTAC
 441 S I Y Q E L P K N P K T S Q Y F F Q L Q B H F V K Q D L V G P G P F T V E A P
 1441 CAACGGCTTTGTGAGGAGCTGGGTTAAAGACTGGGACAAATACGGTTTACGGCCCTCTGGTACCATGAGTGTGAGCAGGATTCTGGAAACCTGAAATTGATC
 481 A C P D E B A R V K D W D L M B O V L R Y H V V A C H Q L L E N N K L I
 1561 TCAATGCTACTTCCCTCAAGGAGGACCAATAGTCATCTGGCTCTCTGGAGCAGGTTATATAAACATAAGCTAATGCTATCCAGTGTATCATCAGTACTANTGGAGTTG
 521 S N A T S L Q G E P I V I S V S Q S T V Y I N N K A K I I S S D I T S T N G I V
 1681 CATACATAGACAAATTGCTATCTCCAAAAATTGCTATCACTCCAAAGACAACTTGAGAAGAAATTCTGCAACACATGGCTACATCAAATTGAG
 561 H I D K L L S P K N L I T P K D N N S G R I L Q N L T A T N G Y I K F S
 1801 AACCTAAACAGGACTCAGGTTGCTGAGTGTCTACCGGATCCCCTACCAACCCAGTCAGTCCTCTGGCCACCCGACCTGGCTACCTGGTCAACACAGGACTC
 601 N L I Q D S G L L S V I T D P I H T P V T L F W P T D Q A L H A L P A B Q Q D F
 1921 CTGCTGACCAAGAACAAAGGACAGGAGTGAAGGAGATTGAGATCTGCTGAGTACCGGAGTGGCAAGGTTCTGGTACCTCTCCACATGGCTCGAGAACCCCTGANGT
 641 L F N Q D N K D K L K T E Y L K F H V I D A K V L A T V D L P T S T A W K T L Q
 2041 TCAGAGCTGACTGTGAAATGGAGCTGGCAGGGACATCGGTGACCTCTTGTGAAATGGCCAACCTGAGAATTGTGAGCAGGGAGCTTGTGTTGACCTGGGCTGGCCTACGG
 681 S E L S V K I C G A G R D I G D L F L N G Q T C R I V Q R E L L F D L G V A Y G I
 2161 GACTGCTCTGAGTGTGACCTCCACCTGGGGGGGGCTGTGAGACCTTTACTACTTCGATGGCTGGGGAGTGTGAGTCAACTCCAGGCCAGGAGTAAACCC
 721 D C C L L T P L G G R C D T F T T A T F D A S G E C C G S C V N T T P S C P R R S K P
 2281 AACGGTGTGAAGCAGAAGTGTCTACACCTGCCCTCAAGAGGAACCTGGAAGGCTGCCGGAGCGCTGGTACAGATCCCAGGTGCTGCCAGGCTTCTGGGG
 761 K G V K Q K C L Y N L P F K R N L E G C R E R C S L V I Q I P R C C K I C Y F G R
 2401 GACTGTCAGGCTGCCCTGGAGGACAGATGCCCTGGTAAATAACCGGGGTTCTGCCCTGTGAGTACTCGGACCCGGAGAGTGAATGCAACACCCGCTTCATGGACAGGGCT
 601 D C Q A C P G G P D A F C N N R G V C C L E D D Q Y S A T T G E C K C N T T G F T A C
 2521 GAGATGTCTGGCCGGGGAGATTGGGCTGATTGTCTGCCCTGTGCTCAGACCGACAGTGTGATGAGTATCACGGCTCCGGCAGTGTGAAACGGGG
 841 E M C W P G R F G P D C L P C G C S D R H G Q C D D G I T G S G Q C L C B T G W T
 2641 GGCCCCCTGTGACTACAGGCACTGGCTCTGGAGTGTGAGCTGGCTCTGGTACGGCTCTGGTACGGCACTGTGAAAGGAGAACACAGCTGTGAGTGAACCTGGATTATGAGGTGAGG
 881 G P S C D T Q A V L P A V T C T P P C S A H A T C K E N N T C E C N L D Y E G D G
 2761 ATCACATGACAGTGTGGATTCTGCCAACAGGGGCTGTGCAAGGAGGGCTGAGTGTCCCAGAGGAGCTGGCTCTGGCAGCTGCCAGGAGAAGGGATAACAGGGGAC
 2881 GGGCACAGCTGCACAGGAGTAGACCCCTGTCAGGCCCTAACGGAGGTTGACAGGAGGCCACCTGTAAGATGACAGGCCGGGACACCAACAGTGTGAGTAAAGTCACTAT
 961 G H S C T E I D P C A D G L N G G C H E R A T C K M T G P G K H K C E C K S H Y
 3001 GTGGCAGATGGCTGCACTGGCTGAGCTGGCCAGCTGGCTTACAGGCAATGGGAGTGGCACTGGCAGGCCAATGTGTCAGGCCACTTCCAGGATACCACTGG
 1001 V G D G L N G Q C H A D A K C V D L H F Q P D T V
 3121 GGGGTGTTCCATCTACCTGCCACTTGAGGAGTGTGCTGACCTTGTGACAAACCCAGGGCTGCTGCCAGGAGACCTGGCTCTGGCTGGGATAGTGGACTATGGACCT
 1041 G V F H L R S P L G Q Y K L T F D K A R I E A C A N E A A T M A T Y N Q L S Y A Q
 3241 AAGGCCAAGTACCCACTGTGCTCAGCAGGGCTGGAGACCCGGGGTTGCCATCCCCAACGGCTTCTGCCAGAACACTGGCTCTGGTCTGGGATAGTGGACTATGGACCT
 1081 K A K Y H V I S R P L K A P P V T L T H T G L G A G I F F A I I L V T G A V A L
 3361 AGACCAACAAAGAGTGAATGTGGGATCTCTCTGATCAAAGATGTGACCTGCCACAGGCTGGGCTATGGGAGATGGCTCTGAGTGGCACTGCCAGGCT
 1121 R P N K S E M W D V F C Y R M K D V N C T C K V G Y V G D G F S C S G N L L O V
 3481 CTGATGCTCTCCCTCACTCACAAACTCTGGAGCTGGCCCTATCCACAGCTGGCCCTAGCTGAGGCTGCTTCTAGAACACCTGACTGACCTGCTCCAGG
 1161 L M S F P S S L T N F L T E V L A Y S N S S A R G R A F L D L S I R G T
 3601 TTGTGCCACAGAACAGTGGCTGGGGAGATGAGACCTTGTCTGGGGGACATCGAGCACCCACTGCCAATCTGAGCATTTCTAGAACACCTGACTGACCTGCTCCAGG
 1201 F V P Q N S G L G E N E T L S G R D I E H H L A N V S M F F Y V N D L V N G T T L
 3721 CAAACAGGGCTGGGAAGCAGTGTCTACAGGCCAGGACCTCCAAACCCAGGGAGACAGGTTGGTACGGAGAGGCCATTCTGAGCATCTGGCTCTGG
 1241 Q T R L G S K L S Q D P L Q P T E T R F V D G R A I L Q W D P A S N G
 3841 ATCATTCTGTCATTTCCAGGCCCTTAAAGCACCCCTGGCCCTGACTCTGGAGGACCATCTGGCTCTGGAGGACAGGTTGGTACGGAGAGGCCATTCTGAGCT
 1281 I I T H V I S R P L K A P P V T L T H T G L G A G I F F A I I L V T G A V A L
 3961 GCTGGTACTCCACTTCGGATAAACCGGAGAACATCAGGCCCTGGAGGACATTTGAGTGGAGAGGCAATTAGTGTGAGCTGGCAAGCAGCAGGCCCTGG
 1321 A A Y S Y F R I N R R T I G F Q H F E S E D I N V A A L G K Q Q P E N I N P
 4081 TTGTATGAGAGCACAACCTCAGCTCCCCAGAACCTTCTACAGGCCCTACGGACTCTGAGAGAACGGCAGCTTGAGGGCAATGCCCTTGAGGACACTGAGGG
 1361 L Y E S T T S A P P E F S Y D P F T D S E E R Q L E G N D F L R T L * (1394aa)

Figure 34

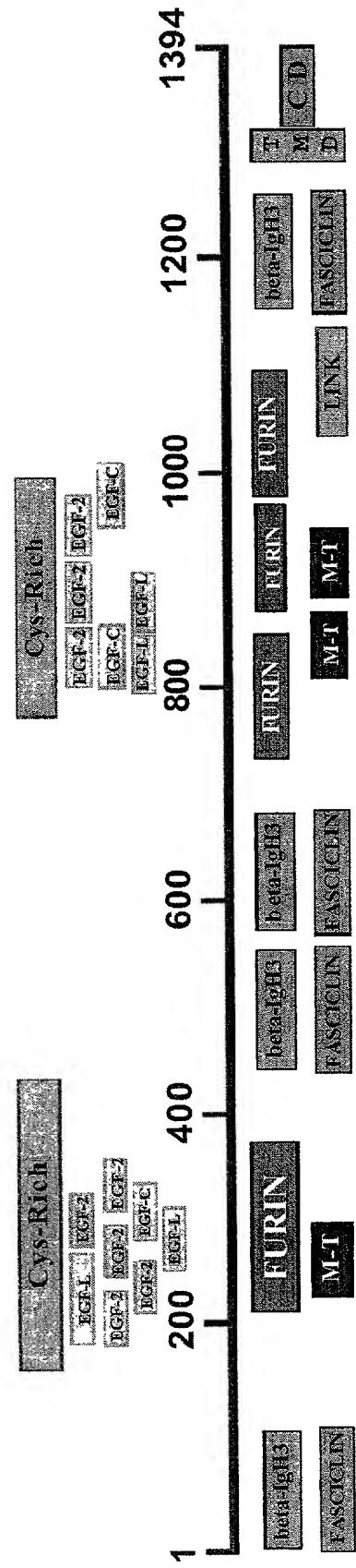


Figure 35

hHARE 1 IGYNLANIAEAADAYTVFAP NNNAAIENYIREKKVLSLEED VLRYHVVLEEKKLLKNDLHNG MRETMGLGSYFLSFEFLHND OLYYNEAPINNTNVATDKGV
 rHARE 23 IHNLASAIESADAYTVFVP NNEAIIENYIREKKATSLKD IIRYHVVLGEKKLLKNDLHNG MRETMGLGSYFLAFLRND QLYYNEAPINNTNVATDKGV
 hHARE 101 IHGIGRKVLEIOKNIDNDA TIIRGRIRT SSELTPFGT KSLGNKEKRR ITYSYFMGRR TLFIG QPK VRTVITRE C AGFTFGPQCOPCPGNAQNVCF
 rHARE 123 IHGLEKVLEIOKNIDNDA IIVRGEGK SQSAPP PLET KPL-RETRK IISIYFMGRR SVFIG QPK VRTVITRE C AGFTFGPQCOPCPGNAQNVCF
 hHARE 201 GNGICLDGVCGVFELEG FSGTAETTEGKYGIHDQ ASVHGRNQGPLGDGSID DVGMWRGH DNAATTEDN C HTISAN LTNSDGTAISK
 rHARE 222 GTASWWDGVCGVFELEG FNGTAETTEGKYGIHDQ ASVHGRNQGPLGDGSID DVGMWRGVK DMEITTDN C HTISAN LLDPDGKASK
 hHARE 301 AAAGFOGNCITATNAEI SNGGSAKAD KRTPGRRV ITKAGYTDGDIV LEINP LENHGG DKNAE TOTGENO AAI LPAYTGDKV TLIN
 rHARE 322 AAAGFRGNCITATNAET SNGGSTKAD KRTPGNRV V KAGYTDGDIV LEINP LENHGG DRNAE TGTGPNQ AVN LPKYTGDKV SLIN
 hHARE 401 VILPKNGG SEFAI HAW Q VERT T KPNYIGDGFTRG SIYQELPKNPNTSQYFFQLQ EHFVKDLVGPGPPTVFAPLS AAFDEBARVKDWKYLGLMPO
 rHARE 422 VILTNNGG SPFAT HAW Q DORIT KPDYTGDITVRG SIYQELPKNPNTSQYFFQLQ EHARVELLAAGPGPPTVFAPLS SSENHEPRIKDMQQGLMSQ
 hHARE 501 VLRYHVVA HOLLLENILKLI SNATSLQGEPIVISQSSTV YINNKAKI LISSDI LISTNGIV HILDKLSPKNLLITPKDNS GRILQNTTLATNINGYIKES
 rHARE 522 VLRYHVVG QQLLDNIRKT TSATTLQGEPVSIQSQDTV FINNEAKVLSSEDI LISTNGIV HVIDKLSPKNLLITPKDAL GRVLTNTVAANHGYTKFS
 hHARE 601 NLIODSGLLSVITDPIHTPV TLFWPPTDOALHALPAEQODF LFNOQNNDKLFKEYLKFKHIVR DSKVALADLPLRSASWKTQLQ SELSYV GAGRDIIGDLEFLNG
 rHARE 622 KLIQDSGLLSVITDHSIPV TVFWPPTDKALEALPEQQDF LFNOQNNDKLFKEYLKFKHIVR DSKVALADLPLRSASWKTQLQ SELSYV GTGSDIGELLINE
 hHARE 701 QT RIVQREPLLFDLGAYGI DLLIDPTLGRIDFTTFD ASGE GS VNTPS PRWSKP KGVKQKLYN-LPFKRNLG RER SLVIQIPR KGYFG
 rHARE 722 QMRFTHRGGLFDVGAYGI DLLMNPTLGRIDFTTFD IPEGEGS LTPKPK PLKSKP KGVKKK VNPPLFRRNVEG QNL TVVIQTPR KGYFM
 hHARE 800 RD QA PGGPDDAPNNRGV LDQYSATGEK INTGFMNTA EM WPGRFEGD LPGCSD HQODDGITGSGQI ETGW TGPSPDTOAVLPAYTPPI
 rHARE 822 PD QA PGGPDTPPNRRGM RDLYTPMGQLHTGFNGA ELL WHGRFEGD QPRS SE HQQ DEGITGSSE L ETGW TAAS DTPTAVFAV TPAS
 hHARE 900 AHAT KENT E NLDYEGD GIT TTVDF KODNNGGAKV AR SQKGTKVSS QKGYKG DGHS TEIDP ADGLNGG H EHAT KMTGPGKH E KSH
 rHARE 922 WHAT TENG V NILNYEGD GIT TTVDF KQNNGGAKV AR SQKGTVQS S KKGYKG DGYS TEIDP ADGVNGG H EHAT RMTGPGKH E KSH
 hHAR 1000 YVGDLN EPEQLPIDRLQ DNGQHADAKVDLHFQDTT VGFVHLRSPQGQKLTFDKA REA ANEAATMAYNQLSYA QKAYHL SAGMLETGRVAY
 rHARE 1022 YVGDGVD EPEQLPLDRLQ DNGQHFDAS ADLYFQDTT VGFVHLRSPQGQKLTFDKA KEA AKEAATLATYNQLSYA QKAYHL SAGMLETGRVAY
 hHARE 1100 PTAFAISON GSGVVGIVDYG PRPNKSEMWDVF YRMKDV SRANK SEMWDVF YRMKDV K VKGYVGDFES SGNLLO VLMSPSLTNFLTEVLAYSN SSARGRAFLEHLDLSIRGT
 rHARE 1122 PTTVASQK GANVVGIVDYG K VKGYVGDFES SGNLLO VLMSPSLTNFLTEVLAYSN SSARGQAPFLKHLTDLSIRGT
 hHARE 1200 LFVPONSGLGENETLSSGRDI EHHLANVSMFYNDLVNET LQTRLGSKLLITASQDPLQ TETRFVDRAILONDIFASN GITHVTSRPLKAPPAPVTLT
 rHARE 1222 LFVPONSGLPGNKSLSGRDI EHHLTNVNSFYNDLVNET LRTMLGSQLLITPSQDLHQ -ETRFVDRGRSLQMDIAAN GILHIISEPLRAPTAATAA
 hHARE 1300 HTGIGAGTFAILVIGAVAA LAZYSPFRINRTIGFOIFIE SEDINVAALGKQOPENISN PLVESTSAPPESD PFTD SEEQRQLEGNDPLRTL
 rHARE 1321 HSGLGNGIFCAVVLVTGAA LAAYSFRUKORTNGFORFD QRRTLMSWLASSSPRISE LCMRPQRHRPOSPPVPSQT LENRIWRTATLWGHCPDMR
 rHARE 1421 SQQATTVTVPR

Figure 36

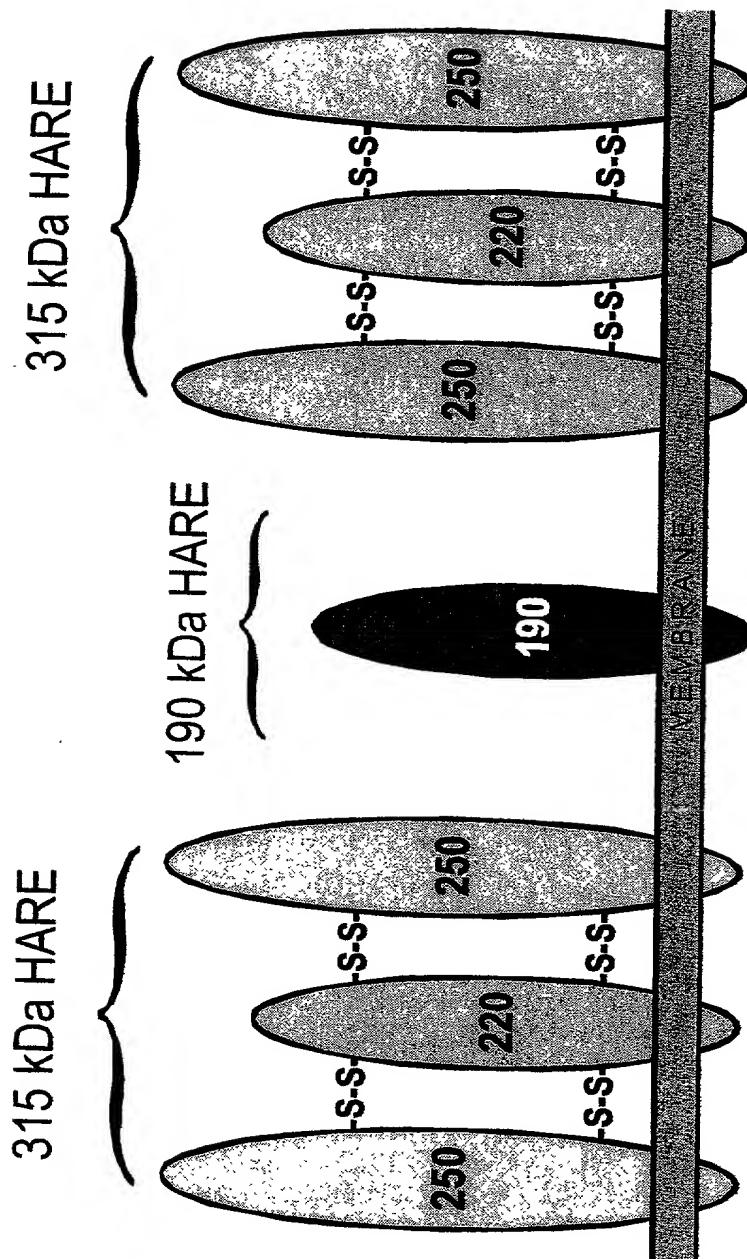


Figure 37

Amplification of the 1394 amino acid HARE
Open Reading Frame from a human lymph
node cDNA Library

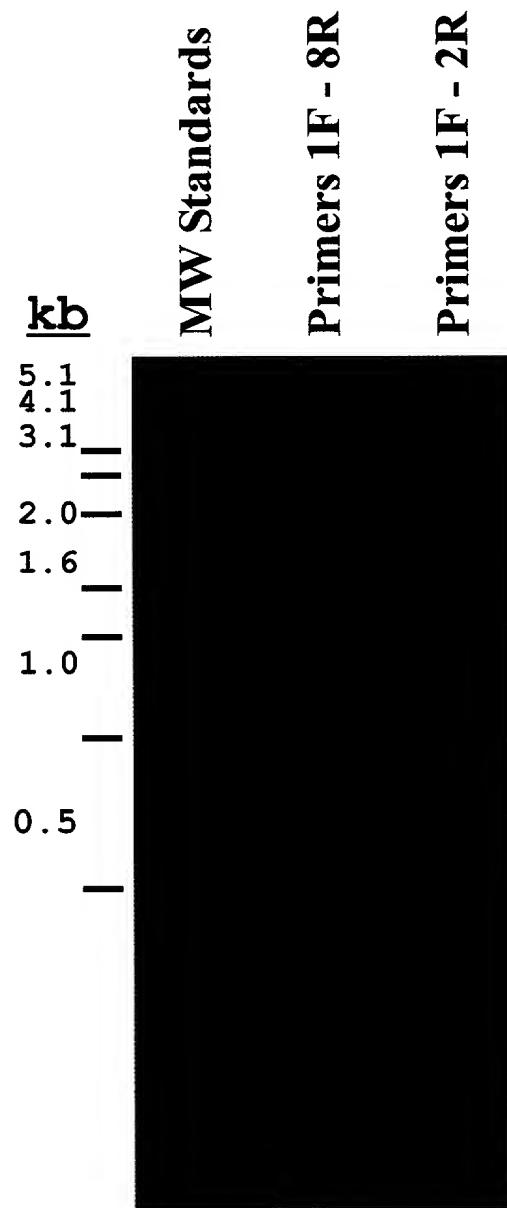


Figure 38

Schematic Organization of the Human HARE Gene on Chromosome 12
(encoding 1357 of the 1394 amino acids disclosed here)

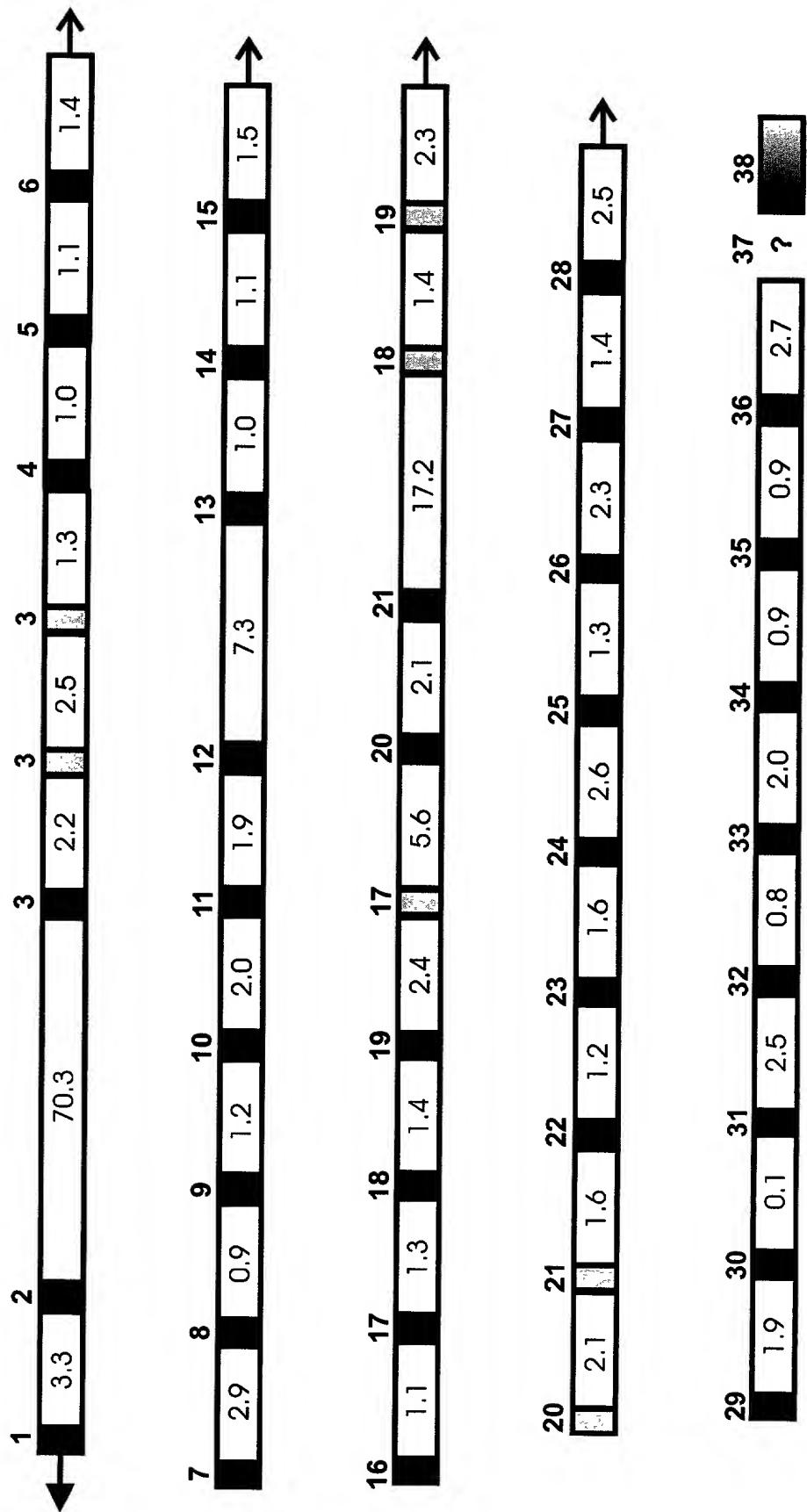


Figure 3 9

